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December 16, 2002, 17:15:32 ; Search time 38 Seconds (without alignments) 1230.815 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 METNFSIPLNEYEEVSYESA......INDIAANSASPPAETELQAM 351
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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1817
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                                                                                                                                                                                                                                                                                                                          Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Title:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Human formyl pepti	Non-endogenous hum	Non-endogenous hum	Mouse protein homo	G-protein coupled	G-protein coupled	Human G protein-co	Human mutant G pro	Mouse C3a receptor	Mouse anaphylatoxi
QI QI	AAU79035	ABB56354	ABB56353	AA021656	AAR48713	AAW02685	AAY90678	AAY90683	AAY72389	AAU75166
DB	23	22	22	23	15	17	21	21	22	23
Length	351	351	350	343	315	315	356	356	477	477
Query e Match Length DB ID	100.0	7.66	68.5	63.7	61.5	61.5	30.5	30.5	29.9	29.9
Score	1817	1811	1244.5	1157.5	1117	1117	554.5	553.5	542.5	542.5
Result	П	7	e	4	S	9	7	80	6	10

Kidney injury asso	Novel G-protein co	Homo sapiens C3a r	Human anaphylotoxi	Human G-protein co	C5a-like seven tra	Human polypeptide,	Non-endogenous hum	Human brain expres	Human bone marrow	Peptide #2450 enco	Peptide #2554 enco	Non-endogenous hum	Lung cancer associ	Human G-protein re	Human Th2/B19. Ho	Human G protein-co	Human G-protein re	Human mutant G pro	Human G-protein re	Human G-protein re	G-protein coupled	G-protein coupled	Recombinant high a	IL8-R type 2-GBP 1	Gorilla CXCR2 rece	Human interleukin	Human IL-8 recepto	Human IL-8 recepto	Human CXCR2 recept	Chimpanzee CXCR2 r	Human G protein co	Protein of the ang	Human Anglotensin	Sequence in a low
AAW86323	AAW23367	AAW42376	AAU99102	AAW02151	AAW06540	AAM93557	ABB56337	AAM55822	AAM68196	AAM16016	AAM28517	ABB56336	AAB58319	AAU01300	AAW44703	AAY90609	AAU01299	AAY90643	AAU01301	AAU01302	AAR48714	AAW02686	AAR80953	AAR70124	AAU80485	AAU10558	AAR33420	AAB09990	AAU80482	AAU80483	AAB02844	AA020951	AAU78654	AAR28273
20	18	19	23	17	18	22	22	22	22	22	22	22	21	22	19	21	22	21	22	22	15	17				23								
372	482	482	482	482	482	355	350	363	363	363	363	482	485	355	395	355	355	355	355	355	304	304	360	1064	355	360	355	355	355	355	359	359	359	360
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542	509.5	509.5	509.5	508.5	508.5	208	507	507	507	507	507	506.5	504.5	n	499.5	499	499	497	496	491	479	479	431.5	430.5	28	427.5	56			426.5		426.5	426.5	
11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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Human; FPRL-1; formyl peptide receptor like-1; receptor;
ILM receptor; macrophage surface receptor; antiinflammatory; pulmonary;
chronic inflammatory airway disease; chronic bronchitis;
chronic obstructive pulmonary disease; COPD.
                                                                                                                                                                                                                                                                                                                    Seither P, Quast K;
                                                                                          Human formyl peptide receptor like-1 receptor, FPRL-1.
                                                                                                                                                                                                                                                                                                                   Mueller S, Kistler B,
                                                                                                                                                                                                                                                                                           (BOEH ) BOEHRINGER INGELHEIM PHARMA KG.
                     AAU79035 standard; Protein; 351 AA.
                                                                                                                                                                                                                                                                   01-SEP-2000; 2000GB-0021484.
                                                                                                                                                                                                                                               23-AUG-2001; 2001WO-EP09727.
                                                                18-JUN-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-315580/35.
N-PSDB; ABK48101.
                                                                                                                                                                                                                                                                                                                   Kraut N,
                                                                                                                                                                                                WO200218938-A1.
                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                       07-MAR-2002.
                                             AAU79035;
                                                                                                                                                                                                                                                                                                                   Jung B,
Weith A;
RESULT 1
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The invention relates to determining an expression level of an ILM receptor (macrophage surface receptor), comprises determining the level of an ILM receptor expressed in a macrophage. Also included are a method of determining whether a substance is an activator or an inhibitor of an ILM receptor, involving applying the substance to a test system which compressed in that the substance to determining whether a substance is an activator or an inhibitor of an ILM receptor function, a test system for determining whether a substance is an activator or an inhibitor of an ILM receptor function, a test system for determining whether a substance of alway disease and where the receptor is involved in a chronic inflammatory airway disease and where the receptor is an expression vector capable of expression vector capable of expression vector capable of expression vector capable of expression of the ILM receptor and a substance determined to be an activator or inhibitor of an ILM receptor, is useful for treating constructive pulmonary disease, e.g. chronic bronchitis and chronic of the diseases and for modilating an ILM receptor, is useful for treating the present sequence is an ILM receptor which is differentially expressed and which is involved in causing the induction and/or in an anti-armaly disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
Determining an expression level of ILM (a macrophage surface receptor), for the diagnosis or monitoring of chronic inflammatory airway disease, comprises determining the level of the ILM receptor expressed in a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 1817; DB 23; Length 351; 100.0%; Pred. No. 9.5e-196; 1.1ve 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LYVFVGQDFRERLIHSLPTSLERALSEDSAPTNDTAANSASPPAETELQAM 351
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                                                                                          Claim 7; Page 49-51; 79pp; English.
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The invention relates to G protein-coupled receptors (GPCRs) for which the endogenous ligand has been identified. Non-endogenous constitutively activated versions of known GPCRs are used in the invention for the direct identification of candidate compounds as receptor agonists, inverse agonists or partial agonists. Such agonists are useful as therapeutic agents for diseases or disorders version of a known human GPCR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Identifying agonists of G protein-coupled receptors (GPCRs) for u disease treatment, comprises contacting candidate compounds with versions of GPCRs -
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1811; DB 22;
Pred. No. 4.5e-195;
constitutively activated GPCR; agonist; disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                       Claim 1; Page 301-302; 394pp; English.
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                                                                                                                                                                                 Liaw CW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 99.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            99.78;
                                                                                                                                  07-APR-2000; 2000US-195747P.
                                                                                                         05-APR-2001; 2001WO-US11098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 350; Conservative
                                                                                                                                                        (AREN-) ARENA PHARM INC
                                                                                                                                                                                Lehmann-Bruinsma K,
                                                                                                                                                                                                       2001-648759/74
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                         351 AA;
                                                                                                                                                                                                                   N-PSDB; AB197990
                                                         WO200177172-A2
                       Homo sapiens.
                                                                                 18-OCT-2001
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                                    Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                  Identifying agonists of G protein-coupled receptors (GPCRs) for udisease treatment, comprises contacting candidate compounds with versions of GPCRs -
                                          Human; G protein-coupled receptor; GPCR; non-endogenous; mutant;
constitutively activated GPCR; agonist; disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68.5%; Score 1244.5; DB 22; Length 350;
68.6%; Pred. No. 2.8e-131;
ive 37; Mismatches 72; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LYVFVGQDFRERLIHSLPTSLERALSEDSAPTNDTAANSASPPAETELQA 350
               Non-endogenous human GPCR protein, SEQ ID NO: 499.
                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 299-300; 394pp; English.
                                                                                                                                                                                                                                                                              Lin I;
                                                                                                                                                                                                                                                                              Liaw CW,
                                                                                                                                                                                       05-APR-2001; 2001WO-US11098.
                                                                                                                                                                                                                    07-APR-2000; 2000US-195747P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 240; Conservative
                                                                                                                                                                                                                                                 (AREN-) ARENA PHARM INC.
                                                                                                                                                                                                                                                                            Lehmann-Bruinsma K,
                                                                                                                                                                                                                                                                                                        WPI; 2001-648759/74.
N-PSDB; ABI97989.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Theal Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          350 AA;
                                                                                                                              WO200177172-A2.
                                                                                      sapiens
                                                                                                                                                           18-OCT-2001
                                                                                                    Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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                                                                                      Homo
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The invention relates to isolated polynucleotides encoding Musculus FMRL-3 proteins. The M. Musculus FMRL-3 polynucleotides and their vector may be used in a process for producing the FMRL-3 polypeptides by recombinant techniques in a host cell. The FMRL-3 polypeptides may be used in assays for screening for compounds that either agonise or antagonise M. Musculus FMRL-3. The compounds identified are useful in the treatment of human diseases e.g. infections such as bacterial, the treatment of human diseases e.g. infections such as bacterial, chugal, protozoan and viral infections (particularly infections by Human consist, and mundeficiency Virus (HIV)-1 or HIV-2), pain, cancers, diabetes, consist, any apportancy virus (HIV)-1 or HIV-2), pain, cancers, diabetes, obseity, anoteration, hypertension, urinary retention, osteoporosis, angina pectoris, myocardial infarction, stroke, ulcers, allergies, benign constant hypertension, infanction, stroke, ulcers, allergies, benign constant hopperstophy; migraline, vomiting, psychotic and neurological depression, delirium, dementia, and severe mental retardation) and dyskinesias (such as Huntington's disease or Gilles de la Tourett's syndrome). The polynucleotides and proteins of the invention can be used in the treating of disorders by gene therapy, protein therapy and the treating of disorders by gene therapy, protein therapy and the treation. This sequence represents a mouse protein with homology to
                                                                                                                                              Antibacterial; fungicide; protozoacide; virucide; anti-HIV; analgesic; cytostatic; diabetes; anorectic; anabolic; antiasthmatic; cardiovascular; antiparimoniam; hypotensive; hypertensive; renal; antibulcer; relaxant; osteopathic; antianginal; antischemic; antiallergic; antimicarine; antidepressant; anticonvulsant; FMRL-3v; FMRL-3; HIV-1; HIV-2; pain; cancer; diabetes; obesity; anorexia; bullmia; asthma; urinary retention; Parkinson's disease; acute heart failure; hypotension; hypertension; osteoporosis; angina pectoris; myocardial infarction; stroke; ulcer; allergy; benign prostatic hypertrophy; migraine; vomiting; psychotic; neurological disorder; anxiety; schizophrenia; manic depression; delixium; dementa; severe mental retardation; dyskinesias; gene therapy; Huntington's disease; Gilles de la Tourett's syndrome; protein therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isolated polynucleotides encoding Mus Musculus FMRL-3v, useful for identifying compounds for treating e.g. cancers, Parkinson's diseases and depression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 23; Length 343;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5,
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                                                                                                           Mouse protein homologous to Mus musculus FMRL-3 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63.7%; Score 1157.5; DB 23
65.8%; Pred. No. 1.7e-121;
ive 39; Mismatches 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the Mus musculus FMRL-3 protein of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-JUN-2001; 2001US-0879017.
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                                                               05-SEP-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   vaccine; mouse; murine.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 229; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            343 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-APR-2002.
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AA021656 standard; Protein; 343 AA.

AA021656 ID AA02 RESULT 4

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Gaps 86 9

10;

Length 315; Indels 146

206

266

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---HWPFGWFLCKFLFTIVDINLFGSVFLIALIALDRCVCVLHPVWTQNHRTVSLAKKVI 117
                                                                                                                                                                                                                                                                                                           WLKEMLFYGKYKIIDILVNPTSSLAFFNSCLNPMLYVFVGQDFRERLIHSLPTSLERALS 326
GPR abnormality e.g. a psychotic disorder such as schizophrenia.
                                                                                                                                           27 ILPLVVLGVTFVLGVLGNGLVIWVAGFRMTRTVTTICYLNLALADFSFTATLPFLIVSMA
                                                                                                                                                             MGEKWPFGWFLCKLIHIVVDINLFGSVFLIGFIALDRCICVLHPVWAQNHRTVSLAMKVI
                                                                                                                                                                                                                                                                                                                                                           207 VIGFSLPMSIVAICYGLIAAKIHKKGMIKSSRPLRVLTAVVASFFICWFPFQLVALLGTV
                                                                                                                                                                                                                                                                                                                                                                                 147 VGPWILALVLTLPVFLFLTTVTIPNGDTYCTFNFASWGGTPEERLKVAITMLTARGIIRF
                                                                    61.5%; Score 1117; DB 15;
67.3%; Pred. No. 5.5e-117;
11ve 37; Mismatches 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92US-0943236
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92US-0943236.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                  Query Match
Best Local Similarity 67.3%
Matches 218; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1996-208785/21.
                                     315 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
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10-SEP-1992;
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                                   Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          G-protein coupled receptor; ligand binding assay; transmembrane domain; psychotic disorder; schizophrenia; dopamine; cAMP; adenosine; thrombin; muscarinic acetylcholine; adenomergic; endothelin; bombesin; endocrine; rhodopsin; opsin; odorant; cytomegalovirus.
                                                                                                                                                        LDRCICVLHPVWAQNHRTVSLAMKVIVGPWILALVLTLPVFLFLTTVTIPNGDTYCTFNF 180
                                                                                   61 TICYLNLALADFSFTATLPFLIVSMAMGEKWPFGWFLCKLIHIVVDINLFGSVFLIGFIA 120
                                                                                                                                                                                                                                                                                                     RVLTAVVASFFICWFPFQLVALLGTVWLKEMLFYGKYKIIDILVNPTSSLAFFNSCLNPM 300
                                                                                                                                                                                                                                                                                                                        241 RVLTAVAISFFMCWFPFQLIILLGNIWNKE----TPSSIHILLNPASTLASFNSCLNPI 295
                                                  9
                9
                                                                                                        181 ASWGGTPEERLKVAITMLTARGIIRFVIGFSLPMSIVAICYGLIAAKIHKKGMIKSSRPL
              METNFSTPLNEYEEVSYESAGYTVLRILPLVVLGVTFVLGVLGNGLVIWVAGFRMTRTVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polypeptides of G-coupled receptor proteins (GPRs) - useful for binding GPR ligands or modulating GPR binding
                                                                                                                                                                                                                                                                                                                                                                        301 LYVFVGQDFRERLIHSLPTSLERALSEDSAPTNDTAANSASPPAETEL 348
                                                                                                                                                                                                                                                                                                                                                                                          G-protein coupled human N-formyl peptide receptor protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 87-88; 160pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR48713 standard; Protein; 315 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-JUN-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schuster DI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1994-101120/12.
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AAR48713;

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Proteins AAW02657-W02730 represent a range of G-protein coupled receptor (GPR) proteins selected from cAMP, adenosine, muscarinic acetylcholine, adrenergic, thrombin, endothelin, bombesin, endocrine, rhodopsin, opsin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            G-protein coupled receptor; ligand binding assay; transmembrane domain; schizophrenia; dopamine; cAMP; adenosine; thrombin; adrenergic; opsin; muscarinic acetylcholine; endothelin; bombesin; endocrine; rhodopsin;
New dopamine receptor peptide - useful as antipsychotic agent, for treating schizophrenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      G-protein coupled human N-formyl peptide receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Column 97-100; 184pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  odorant; cytomegalovirus; serotonergic.
                                                                                                                                                                                                                                                                                                                                                                                                 AAW02685 standard; peptide; 315 AA.
                                                                                                                      EDSAPTNDTAANSASPPAETELQA 350
                                                                                                                                                           ||| |:||| || ||| EDSTQTSDTATNSTLPSAEVALQA 314
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odorant, cytomegaloviral and other GPR proteins. The receptor proteins were used to design polypeptides, pref. based on the transmembrane domains, for use in G-protein coupled receptor ligand binding assays. The polypeptide fragments retain biological activity such as binding a GRR ligand or modulating GPR ligand binding to a GPR (see AAW02747-W02999 for examples of polypeptide fragments. The polypeptide fragments can be used in compositions for treating subjects suffering from a pathology related to a GPR abnormality e.g. a psychotic disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     87 MGEKWPFGWFLCKLIHIVVDINLFGSVFLIGFIALDRCICVLHPVWAQNHRTVSLAMKVI 146
                                                                                                                                                                                                                                                                                                                                                                                      207 VIGFSLPMSIVAICYGLIAAKIHKKGMIKSSRPLRVLTAVVASFFICWFPFQLVALLGTV 266
                                                                                                                                                                                                                                                                                                                                                                                                                                              267 WLKEMLFYGKYKIIDILVNPTSSLAFFNSCLNPMLYVFVGQDFRERLIHSLPTSLERALS 326
                                                                                                                                                                                                                                                                                                                          ---HWPFGWFLCKFLFTIVDINLFGSVFLIALDACVCVLHPWWTQNHRTVSLAKKVI 117
                                                                                                                                                                                                                                                                                                                                                                 147 VGPWILALVLTLPVFLFLTTVTIPNGDTYCTFNFASWGGTPEERLKVAITMLTARGIIRF 206
                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                              27 ILPLVVLGVTFVLGVLGNGLVIWVAGFRMTRTVTTICYLNLALADFSFTATLPFLIVSMA 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Non-endogenous constitutively activated human G protein-coupled
                                                                                                                                                                                                                    10;
                                                                                                                                                                                    61.5%; Score 1117; DB 17; Length 315; 67.3%; Pred. No. 5.5e-117; ive 37; Mismatches 59; Indels 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               G protein-coupled receptor; GPCR; constitutively active; intracellular loop 3; transmembrane domain 6; drug screening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human G protein-coupled receptor GPR32.
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                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Behan DP, Chalmers DT,
                                                                                                                         such as schizophrenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-329165/28.
N-PSDB; AAA30756.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             agonist; antagonist
                                                                                                                                                                                                 Local Similarity
nes 218; Conserv
                                                                                                                                                      315 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200022129-A1
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                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY90678;
                                                                                                                                                                                   Query Match
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Matches
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AAY90677 and AAY90683. Yellow of the inventions virially active the contain a material process. AAY90677 and AAY90683. AAY90687 and AAA90799. The mutant proteins of the invention contain a mutation in a portion of the protein comprising intracellular loop 3 (IC3) and transmembrane domain 6 (TM6). A non-endogenous amino acid, X, is substituted for an endogenous residue in IC3 at a position 16 amino acids N-terminal of an endogenous residue in IC3 at a position 16 amino acids N-terminal of an endogenous proline. In TM6 to form a sequence X-(AA)15-Pro. The endogenous amino acid is selected from Lys, His, Arg or Ala, and is preferably Lys. When the endogenous residue at this position is Lys, this residue is replaced by His, Arg or preferably Ala. The 15 amino acid stretch between the substituted amino acid and the Prompt be endogenous residues. The constitutively active GPCRs are useful for incomposinous residues. The mutant proteins are also useful in research settings for elucidating the roles of the receptors in normal and diseased conditions. Antagonists for a particular GPCR are useful for treating diseases and disorders associated with that receptor. Because the novel mutant GPCRs are constitutively active, they can be used directly for screening of compounds without the need for endogenous lightness. The present sequence represents a human wild-type GPCR referred to in an exemplification of the invention.
                                                                                                                     The invention relates to constitutively active, non-endogenous versions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    217 TIGHFLLGFLGPLAIIGTCAHLIRAKLLREGWVHANRPARLLLVLVSAFFIFWSPFNVV- 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  262 LLGTVWLKEMLFYGKYKIIDILVNPTSSLAFFNSCLNPMLYVFVGQDFRERLIHSLPTSL 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82 IVSMAMGEKWPFGWFLCKLIHIVVDINLFGSVFLIGFIALDRCICVLHPVWAQNHRTVSL 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            202 GIIRFVIGFSLPMSIVAICYGLIAAKIHKKGMIKSSRPLRVLTAVVASFFICWFPFQLVA 261
receptors, useful for identifying agonists for use as pharmaceutical agents -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      142 AMKVIVGPWILALVLTLPVFLFLTTVTIPNGDTYCTFNFASWGGTPEERLKVAITMLTAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25 LRILPLVVLGVTFVLGVLGNCLVIWVAGFRMTRTVTTICYLNLALADFSFTATLP---FL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 554.5; DB 21; Length 356; Pred. No. 1.4e-53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               G protein-coupled receptor; GPCR; constitutively active; intracellular loop 3; transmembrane domain 6; drug screening; agonist; antagonist; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30.5%; Score 554.5, 241.0%; Pred. No. 1.4e-53; tive 59; Mismatches 113; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human mutant G protein-coupled receptor GPR32 (K255A).
                                                                          Example 1; Page 305-306; 341pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY90683 standard; Protein; 356 AA.
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Best Local Similarity 41.0%
Matches 126; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               356 AA;
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Homo sapiens. 12-OCT-1999; 20-APR-2000 Synthetic. Behan DP,

99WO-US23938. 98US-0170496 Chalmers DT, (AREN-) ARENA PHARM INC WPI; 2000-329165/28. N-PSDB; AAA30775. WO200022129-A1. 13-OCT-1998;

Liaw CW;

Non-endogenous constitutively activated human G protein-coupled receptors, useful for identifying agonists for use as pharmaceutical

Example 2; Page 322-324; 341pp; English.

The invention relates to constitutively active, non-endogenous versions of endogenous human orphan G protein-coupled receptors (GPCRs, AAY90643-C AAY90677 and AAX90677 and AAX90677 and AAX90677 and AAX90779-A30779). The mutant proteins of the invention contain a mutation in a portion of the protein comprising intracellular loop 3 (103) and transmembrane domain 6 (TM6). A non-endogenous amino acid, X, is substituted for an endogenous residue in IC3 at a position 16 amino acids N-terminal of an endogenous proline in TM6 to form a sequence X-(AA)15-Pro. The endogenous proline in TM6 to form a sequence CC X-(AA)15-Pro. The endogenous amino acid is selected from Lys, His, Arg or Ala, and is preferably Lys. When the endogenous acid at this position is Lys, this residue is replaced by His, Arg or preferably Ala. The 15 amino acid stretch between the substituted amino acid and the Procomay be endogenous in on-endogenous, or a mixture of endogenous and non-endogenous rane constitutively active GPCRs are useful for identifying antagonists, agonists and partial agonists for use as phramaceutical agents. The mutant proteins are also useful in research settings for elucidating the roles of the receptors in normal and settings for elucidating the roles of the receptors in normal and classased conditions. Antagonists for a particular GPCR are useful for treating diseases and disorders associated with that receptor. Because the novel mutant GPCRs are constitutively active, they can be used ligands. Sequences AAY90643-AAY90677 and AAY90681-Y90687 the mutant the hardon of the novel mutant the need for endogenous and manner and the acceptor and any active they can be used ligands. human GPCRs of the invention.

356 AA; Sequence

.. 7 Gaps . 6 DB 21; Length 356; 30.5%; Score 553.5; DB 21; Length 41.0%; Pred. No. 1.9e-53; tive 59; Mismatches 113; Indels Matches 126; Conservative Local Similarity Query Match Best Local S

25 LRILPLVVLGVTFVLGVLGNGLVIWVAGFRMTRTVTTICYLNLALADFSFTATLP---FL 81

å g à

IVSMAMGEKWPFGWFLCKLIHIVVDINLFGSVFLIGFIALDRCICVLHPVWAQNHRTVSL 141 82 g

142 AMKVIVGPWILALVLTLPVFLFLTTVTIPNGDTYCTFNFASWGGTPEERLKVAITMLTAR ò g

202 GIIRFVIGFSLPMSIVAICYGLIAAKIHKKGMIKSSRPLRVLTAVVASFFICWFPFQLVA 261 ö g

262 LLGTVWLKEMLFYGKYKIIDILVNPTSSLAFFNSCLNPMLYVFVGQDFRERLIHSLPTSL 321 ... = á

276 LLVHLWRRVMLKEIYHPRMLLILQASFALGCVNSSLNPFLYVFVGRDFQEKFFQSLTSAL 335 Mouse; OWA protein; obese mice adipocyte; P7P7C1; fuel metabolism disorder; therapy; obesity; diabetes; gene therapy; anorectic; antidiabetic; C3a receptor. AAY72389 standard; Protein; 477 AA. 13-JUN-2000; 2000WO-US16217. Mouse C3a receptor protein. (first entry) (AMYL-) AMYLIN PHARM INC. Sierzega M, Albrandt K; WPI; 2001-112322/12. 322 ERALSED 328 N-PSDB; AAD02458 336 ARAFGEE 342 WO200078950-A2. 24-APR-2001 22-JUN-1999; 28-DEC-2000. AAY72389; Mus sp. RESULT 9 AAY72389 g ð g

The present sequence is mouse C3a receptor protein encoded by a cDNA. The 3' untranslated portion of C3a receptor CDNA corresponds to P7P7C1 cons. A fragment which encodes OMA (obese mice adipocyte) protein. OMA is used as a diagnostic reagent for diagnosing a disorder of fuel metabolism in an underweight or an overweight individual, by detecting the transcription level of a gene encoding OMA, which is induced or repressed in an individual by a factor such as genetic obesity, fasting and refeeding of a fasted individual OMA is useful in the generation of antibodies, for use in pharmaceutical compositions and for studying antibodies, for use in pharmaceutical compositions and for studying enteractions. Nucleic acids encoding OMA are involved in gene therapy. An inhibitor of OMA or an antisense oligonucleotide that inhibits expression of OMA are useful for treating disorders of fuel metabolism such as obesity or diabetes. Novel obese mice adipocyte polypeptides useful in diagnosis and treatment of disorders of fuel metabolism such as obesity or diabetes Claim 11; Fig 9; 83pp; English.

477 AA; Sequence

Gaps 27 ILPLVVLGVTFVLGVLGNGLVIWVAGFRMTRTVTTICYLNLALADFSFTATLPFLIVSMA 86 29.9%; Score 542.5; DB 22; Length 477; 28.1%; Pred. No. 4.8e-52; ive 58; Mismatches 109; Indels 165; Query Match 29.99 Best Local Similarity 28.11 Matches 130; Conservative g

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87 MGEKWPFGWFLCKLIHIVVDINLFGSVFLIGFIALDRCICVLHPVWAQNHRTVSLAMKVI 146 : ||:| ||||| :: :|:| |||||: |:||||| : :QGHWPYGLFLCKLIPSIIILNMFASVFLLTAISLDRCLIVHKPIWCQNHRNVRTAFAIC 143

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147 VGPWILALVLTLPVFLFLTTVTIPNGDTYCTFNFAS--------------------- 182 ò

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Mouse; transgenic; disruption of target gene; disease model; modulation of gene expression; behavioural phenotype; thymus abnormality; seizure; stimulus processing; anaphylatoxin C3a receptor; receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to a method of creating transgenic animals, particularly transgenic anico, computaing a disruption in a target gene. Examples of target genes given in the specification include the mouse anaphylatoxin C3a receptor gene, 5-HT5A gene, chordin gene, RORgamma
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203 TAQLIGHMNDRSAPSSVQARDYFWIVITALQSQPFLITSPEDSFSLDSANQQPHYGGKPPN 262
                                                                                                                                         263 VLTAAVPSGFPVEDRKSNTLNADAFLSAHTELFPTASSGHLYPYDFQGDYVDQFTYDNHV 322
                                                                                                                                                                                              323 PTPLMAITITRLVVGFLVPFFIMVICYSLIVFRMRKTNFTKSRNKTFRVAVAVVTVFFIC 382
                                                                                                                                                                                                                                        WFPFQLVALLGTVWLKEMLFYGKYKIIDILVNPTSS------LAFFNSCLNP 299
                                                                                                                                                                                                                                                                  ------VLLLITDPESSLGEAVMSWDHMSIALASANSCFNP 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel transgenic mouse comprising disruption in target gene e.g., an anaphylatoxin C3a receptor gene, chordin gene, useful for identifying agents that modulate expression or function of target gene
                                                --WGGTPEE 189
                                                                                                                                                                         196 -TMLTARGIIRFVIGFSLPMSIVAICYGLIAAKIHKKGMIKS-SRPLRVLTAVVASFFIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matthews W,
                                                                                                                                                                                                                                                                                                                       426 FLYALLGKDFRKKARQSIKGILEAAFSEELTHSTNCTQDKAS 467
                                                                                                                                                                                                                                                                                                   MLYVFVGQDFRERLIHSLPTSLERALSEDSAPTNDTAANSAS 341
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mouse anaphylatoxin C3a receptor
                                                                                                                                                                                                                                                                                                                                                                                                                 AAU75166 standard; Protein; 477
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29-JUN-2000; 2000US-215462P.
29-JUN-2000; 2000US-215404P.
29-JUN-2000; 2000US-215466P.
29-JUN-2000; 2000US-215466P.
29-JUN-2000; 2000US-215466P.
27-JUL-2000; 2000US-221667P.
26-OCT-2000; 2000US-244083P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-JUN-2001; 2001WO-US20795.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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                                                                                                           190 RLKVAI------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (DELT-) DELTAGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-164479/21.
                                                                                                                                                                                                                                                                      WTPYHLVG----
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gene. BMP gene, airway trypsin-like protease gene and the aquaporin identifying an agent that modulates the expression or function of a gene. The transgenic mice are useful as models for disease and for identifying an agent that modulates the expression or function of a gene. The transgenic mice models are useful for identifying drugs and pharmaceutical therapies. They are also useful for testing and developing new treatments relating to behavioural phenotypes. They are useful for potential treatments for various diseases. For example, a transgenic mouse comprising a disruption in the anaphylatoxin CJa receptor gene is useful for identifying an agent that ameliorates a thymus abnormality, an increased susceptibility to seizure, or a stimulus processing deficit. The present sequence represents mouse anaphylatoxin CJa receptor. The encoding gene is disrupted to produce transgenic mice in the methods of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MGEKWPFGWFLCKLIHIVVDINLFGSVFLIGFIALDRCICVLHPVWAQNHRTVSLAMKVI 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              203 TAQLTGHMNDRSAPSSVQARDYFWTVTTALQSQPFLTSPEDSFSLDSANQQPHYGGKPPN 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 263 VLTAAVPSGFPVEDRKSNTLNADAFLSAHTELFPTASSGHLYPYDFQGDYVDQFTYDNHV 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      323 PIPLMAITITELVVGELVPFFIMVICYSLIVFRARKTNFTKSRNKTFRVAAVVTVFFIC 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             383 WTPYHLVG------VLLLITDPESSLGEAVMSWDHMSIALASANSCFNP 425
                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                              27 ILPLVVLGVTFVLGVLGNGLVIWVAGFRMTRTVTTICYLNLALADFSFTATLPFLIVSMA 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kidney injury associated molecule; kidney injury related molecule; KIM; tissue growth promotion; regeneration; renal condition; acute renal failure; acute nephritis; tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |::| |: :|||: : | : : | : | 14 GCVWVVAFVWCVPVFVY - RDLFIMDNRSICRYNFDSSRSYDYWDYVYKLSLPESNSTDNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24 IASMVILGLICLIGLIGNICVLWVAGVKMKTTVNTVWFLHLTLADFLCCLSLPFSLAHLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          196 -TMLTARGIIRFVIGFSLPMSIVAICYGLIAAKIHKKGMIKS-SRPLRVLTAVVASFFIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    254 WFPFQLVALLGTVWLKEMLFYGKYKIIDILVNPTSS------LAFFNSCLNP
                                                                                                                                                                                                                                                                                                                                                         29.9%; Score 542.5; DB 23; Length 477; 28.1%; Pred. No. 4.8e-52; ive 58; Mismatches 109; Indels 165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            147 VGPWILALVLTLPVFLFLTTVTIPNGDTYCTFNFAS---------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         300 MLYVFVGQDFRERLIHSLPTSLERALSEDSAPTNDTAANSAS 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kidney injury associated molecule HW055 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      190 RLKVAI
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                                                                                                                                                                                                                                                                                                                  477 AA;
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Matches
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The present sequence represents a kidney injury associated molecule

(KIM) protein. KIM proteins can be administered therapeutically
by expressing KIM encoding polynuclecitides, to promote growth and/or
survival of damaged tissue (e.g. renal tissue), since the KIM proteins
curvival of damaged tissue (e.g. renal tissue), since the KIM proteins.

KIM fusion proteins, conjugates, antibodies and vectors can also be used
therapeutically, e.g. these or the KIM proteins may be included with an
acceptable carrier in pharmaceutical compositions, useful for therapy/
prophylaxis of conditions associated with disfunction/disregulation of
KIM genes or proteins, especially renal fallure, acute nephritis). The
polynuclecities can be used to produce antisense sequences which, when
internalised into cells, can disrupt expression of a cellular KIM gene,
clineralised into cells, can disrupt expression of a cellular KIM gene,
also useful in therapy (e.g. to block the growth of tumours dependent on
the prophylaxis of compositions. The proteins and polynuclecities are
useful diagnostically e.g. to detect and quantify renal injury/disease
(indicative of increased risk, or presence of, renal injury or impaired
tissue growth arising from/affecting renal tissue). The proteins can
also be used to locate KIM-producing cells (especially specific loci,
also be used to locate KIM-producing cells (especially specific loci,
also be used to locate KIM-producing/expressing KIM such as tumours
also be used to locate KIM-producing/expressing KIM such as tumours
also be used to locate KIM-producing/expressing KIM such as tumours
also be used to locate KIM-producing/expressing KIM such as tumours
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also be used to locate KIM-producing/expressing KIM such as tumours
also be used to locate KIM-producing/expressing KIM such as tumours
also be used to loc
                                                                                                                                                                                                                                                                                                                                                      Kidney injury-associated molecule, KIM, polypeptides - upregulated in injured or regenerating tissues, useful to promote tissue growth and regeneration, especially to treat renal conditions
                                                                                                                                                                                                           Sanicola-Nadel M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 17; Page 125-126; 213pp; English.
98WO-US10547.
                                                       97US-0047491.
                                                                                                                                                                                                           Cate RL, Hession CA,
                                                                                                                                                                                                                                                               WPI; 1999-045312/04.
                                                                                                                                             (BIOJ ) BIOGEN INC.
                                                                                                                                                                                                                                                                                              N-PSDB; AAV80608.
22-MAY-1998;
                                                          23-MAY-1997;
                                                                                      23-MAY-1997;
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372 AA; Sequence

CYLNLALADFSFTATLPFLIVSMAMGEKWPFGWFLCKLIHIVVDINLFGSVFLIGFIALD 122 RCICVLHPVWAQNHRTVSLAMKVIVGPWILALVLTLPVFLFLTTVTIPNGDTYCTFNFAS 182 RCISVLLPVWSQNHRSVRLAYMTCVVVWVLAFFLSSPSLVFRDTVSTSHGKITCFNNFSL 194 229 HKKGMIKSSRPLRVLTAVVASFFICWFPFQLVALLGTVWLKEMLFYGKYKIIDILVNP-T 287 Gaps 11 EYEE-----VSYESAG---YTVLRILPLVVLGVTFVLGVLGNGLVIWVAGFRMTRTVTTI 62 WGGTPEE------RLKVAITMLTARGIIRFVIGFSLPMSIVAICYGLIAAKI 38; Length 372; 29.8%; Score 542; DB 20; Length 37; 35.5%; Pred. No. 3.9e-52; ive 66; Mismatches 119; Indels Query Match 29.8' Best Local Similarity 35.5' Matches 123; Conservative 63 123 135 183 195 අ õ g Óγ g δ a ŏ g

8 247 QRNRLAKTKKPFKIIITIIITFFLCWCPYH-----TLYLLELHHTAVPASVFSLGLPLA 300 SSLAFFNSCLNPMLYVFVGQDFRERLIHSLPTSLERALSEDSAPTN 333 288 ð g

The present sequence represents a novel G-protein coupled receptor that has an enlarged extracellular loop between the fourth and fifth transmembrane domains. Antibodies generated against the present protein revealed expression in a variety of tissues, including heart, lung and placenta. Diseases or conditions mediated by the G-protein coupled receptor can be treated by administering reagents such as the present sequence, antisense nucleic acid or antibodies generated against the receptor. Reagents may comprise a molecule binding to the creceptor but not transmitting a signal across the cell membrane or reducing effectiveness of binding of the natural ligand. The reagent may also alter the interaction of the receptor with the G-protein with which intracellular domains of the receptor with the G-protein with which intracellular domains of the receptor which can be treated include conditions mediated by the novel receptor which can be treated include gastuma, chronic obstructive pulmonary disease, cystic fibrosis, multiple sclerosis. The antibody can also be used to diagnose these diseases erg. In brain tissue from patients with suspected neurological disease, especially Alzheimer's, in skin samples especially from patients with a suspected inflammatory disease or in haematopoietic cells. The conclude a suspected inflammatory disease or in haematopoietic cells. The expression by standard assays.

Claim 4; Fig 1; 54pp; English.

disease

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Novel G-protein coupled receptor with an enlarged extracellular domain.
                                                                                       G-protein coupled receptor; enlarged extracellular loop; inflammatory disease; asthma; chronic obstructive pulmonary disease; cystic fibrosis; multiple sclerosis; antibody.
                                                                                                                                                                                                                                                                                                                                                                                     G-protein-coupled receptor with enlarged extracellular domain between fourth and fifth transmembrane domains, also nucleic acid and antibodies useful for treating inflammation and neurological
                                                                                                                                                             "predicted N-glycosylation site"
                                                                                                                                                                                                                  /note= "predicted N-glycosylation site"
                                                                                                                                                                                "putative transmembrane domain"
                                                                                                                                                                                                                                    /note= "putative transmembrae domain"
                                                                                                                                                                                                 'note= "enlarged extracellular loop"
                                                                                                                                              Socation/Qualifiers
                  AAW23367 standard; Protein; 482 AA.
                                                                                                                                                                                                                                                                                         97WO-US01736.
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                                                      (first entry)
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                                                                                                                                              Key
Modified-site
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                                                                                                                            Homo sapiens.
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                                    AAW23367;
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RESULT 12
AAW23367
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                                                                                                                                                                                                                                  -----AITMLTARGIIRFVIGFSLPMSIVA 218
                                                                                                                                                                                                                                                                    219 ICYGLIAAKIHKKGMIKS-SRPLRVLTAVVASFFICWFPFQLVALLGTVWLKEMLFYGKY 277
                                                                                                                                                                                                                                                                                                        ---SLAFFNSCLNPMLYVFVGQDFRERLIHSLPTSLER 323
                                                                                        TVTTICYLNLALADFSFTATLPFLIVSMAMGEKWPFGWFLCKLIHIVVDINLFGSVFLIG 117
                                                                                                                          FIALDRCICVLHPVWAQNHRTVSLAMKVIVGPWILALVLTLPVFLFLTTVTIPNGDTYCT 177
                                                                                                                                                                                                               FORPSADSLPRGSARLTSQNLYSNVFKPADVVSPKIPSGFPIEDHETSPLDNSDAFLSTH 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   polyarthritis; systemic vasculitis; multiple sclerosis; Alzheimer's; disease; acute inflammatory disease; Crohn's disease; food; allergies; non-bronchial allergies; osteoarthritis; osteoporosis; thyroid disease; coronary heart disease.
                                    Gaps
                                                    ETN----FSTPLNEYEEVSYESAGYTVLRILPLVVLGVTFVLGVLGVLGVGVTWVAGFRMTR 57
                                                                     7 ETNSTDLLSQPWNEPPV-----ILSMVILSLTFLLGLPGNGLVLWVAGLKMQR 54
                                                                                                                                                            ----MS----
                                                                                                                                                                             174 YKFGLSSSLDYPDFYGDPLENRSLENIVORPGEMNDRLDPSSFQINDHPWTVPTVFQPQT
                 ; Score 509.5; DB 18; Length 482;
; Pred. No. 2.5e-48;
59; Mismatches 117; Indels 193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C3a receptor; treatment; diagnosis; atherosclerosis; chronic;
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                                                                                                                                                                                                                                                                                                                                                    457 AFSEELTRSTHCPSNNVISERNS 479
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                 28.0%;
26.6%;
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                                   Matches 134; Conservative
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                                                                                                                                                                                                                                                                                                        278 KIIDILVNPTS-----
                         Similarity
482 AA;
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 Sequence
                 Query Match
Best Local
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The sequence is that of the C3a receptor. It can be used in a process for diagnosing a disease or susceptibility to a disease related to expression of the C3a receptor. This process involves analysing for the presence of a the C3a receptor in a sample derived from a patient suspected of having such a disease. C3a receptor-related diseases, that can be detected by this method comprise acute inflammatory disease, acherosclerosis, chronic polyarthritis, systemic vasculitis, multiple sclerosis, Alzheimer's Disease, CNS inflammatory disease, Crohn's Disease, food allergies, non-bronchial allergies, osteoarthritis, csteoporosis, thyroid disease, coronary heart disease, Systemic Lupus Erythematosus SLE-associated nephritis, membranoproliferative GN, membranous nephritis, rheumatoid arthritis, Behcet's syndrome, juvenile rheumatoid arthritis, syndrome, myasthenia gravis, cerebral lupus, Guillain-Barre syndrome, pemphigus/pemphigoid, phototoxic reactions, vasculitis, post-bypass syndrome, catheter reactions, sepsis, ARDS, anaphylaxis, transplant rejection, pre-eclamposia, ahreroma, bowel inflammation, thyroiditis, infertility, susceptibility to neisserial infections, recurrent suboutaneous swelling and mucosal oedema, and recurrent episodes of thrombosis/haemolysis. C3a receptor agonists, antagonists and antibodies can be used in the treatment of patients having need to inhibit or activate a C3a receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            294 IKLFPSASSNSFYESELPQGFQDYYNLGQFTDDDQVPTPLVAITITRLVVGFLLPSVIMI 353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      174 YKFGLSSSLDYPDFYGDPLENRSLENIVQPPGEMNDRLDPSSFQTNDHPWTVPTVFQPQT 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   234 FORPSADSLPRGSARLTSQNLYSNVFKPADVVSPKIPSGFPIEDHETSPLDNSDAFLSTH 293
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                                                                                                           C3a receptor agonists, antibodies and antagonists - useful for diagnosis of disease related to expression of C3a receptor, e.g. acute inflammatory disease, atherosclerosis, chronic polyarthritis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----MS-----
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                                                                                                                                                                                                                                                                                                                     Disclosure; Fig 1; 43pp; English.
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WPI; 1998-044336/05.
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                                         N-PSDB; AAV03250
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Matches 134;
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11;

Wed Dec 18 11:07:55 2002

11;

Mismatches 117; Indels 193; Gaps

:65

Conservative

Matches 134;

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the Invention unstables an including the dependent of a pharmaccutically acceptable carrier for use in the manufacture of a pharmaccutically acceptable carrier for use in the manufacture of a medicament for inhibiting, preventing or treating Alzheimer's disease or Parkinson's disease. G protein-coupled receptors are involved in cell carrier and play key roles in cell proliferation, differentiation, allowage in cell carriers. Compositions relating to the anaphylatoxin Ga receptor can also be used against ulcerative colitis, diabetes, myocardial infarction, hypertension, asthma, bronchitis, pneumonia, crown as disease, rheumatoid arthritis, Modkin's lymphoma, glioblastomas and other neurodegenerative disorders. The compositions include and other neurodegenerative disorders. The compositions include antibodies, agonists, antagonists, probes, antisense and gene therapies. The anaphylatoxin Gas acceptor sequence can be used to manufacture medicaments able to reduce symptoms associated with Alzheimer's corrective amount of an Am agonist or antagonist, a pharmaccutically acceptable carrier, adjuvant, excipient, buffer and diluent, and for detecting an increased possibility of Alzheimer's or Parkinson's disease.

The sequence presented is the human anaphylotoxin C3a receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention discloses an isolated and purified composition including the G protein-coupled receptor (GPCR) anaphylatoxin C3a receptor (AR)
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                                                                                                                   AAU99102;
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                                                  RESULT 14
                                                                    AAU99102
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Score 509.5; DB 23; Length 482; Pred. No. 2.5e-48;

28.0%; 26.6%;

Best Local Similarity

Query Match

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Human; C3a; receptor; nootropic; neuroprotective; antiparkinsonian; g protein-coupled receptor; GPCR; anaphylatoxin C3a receptor; AR; Alzheimer,'s disease; Parkinson's disease; cell signalling; proliferation; differentiation; leukocyte migration; que transcription; vision; smell; neurotransmission; hormonal response; ulcerative colitis; diabetes; myocardial infarction; hypertension; asthma; bronchitis; pneumonia; Crohn's disease; rheumatoid arthritis; Hodgkin's disease; glioblastoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isolated and purified composition useful for manufacture of medicament for inhibiting, preventing or treating Alzheimer's or Parkinson's disease, comprises G protein-coupled receptor anaphylatoxin C3a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Roush CL, Morningstar DA;
                                                                                                                                                                                  AAU99102 standard; Protein; 482 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                   Human anaphylotoxin C3a receptor.
457 AFSEELTRSTHCPSNNVISERNS 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (LIFE-) LIFESPAN BIOSCIENCES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-NOV-2000; 2000US-250251P.
30-NOV-2000; 2000US-250452P.
17-OCT-2001; 2001US-330036P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-NOV-2001; 2001WO-US45220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     neurodegenerative disorder.
                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Brown JP, Burmer GC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-508526/54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; ABK86860
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                                                                                                                                                                                                                                                                                                                                         04-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-JUN-2002
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--AITMLTARGIIRFVIGFSLPMSIVA 218 TVTTICYLNLALADFSFTATLPFLIVSMAMGEKWPFGWFLCKLIHIVVDINLFGSVFLIG 117 FIALDRCICVLHPVWAQNHRTVSLAMKVIVGPWILALVLTLPVFLFLTTVTIPNGDTYCT 177 .---SW----- 183 233 234 FORPSADSLPRGSARLTSQNLYSNVFKPADVVSPKIPSGFPIEDHETSPLDNSDAFLSTH 293 ICYGLIAAKIHKKGMIKS-SRPLRVLTAVVASFFICWFPFQLVALLGTVWLKEMLFYGKY 277 396 278 KIIDILVNPTS------SLAFFNSCLNPMLYVFVGQDFRERLIHSLPTSLER 323 54 G-coupled receptor; asthma; transplant rejection; immunodeficiency; ETN----FSTPLNEYEEVSYESAGYTVLRILPLVVLGVTFVLGVLGNGLVIWVAGFRMTR 174 YKFGLSSSLDYPDFYGDPLENRSLENIVQPPGEMNDRLDPSSFQTNDHPWTVPTVFQPQT DNA encoding G-protein coupled receptor - and antagonists and agonists, useful to treat asthma and transplant rejection, and immunodeficiency and severe infections, respectively AAW02151 standard; Protein; 482 AA severe infection; membrane protein. Human G-protein coupled receptor. | | | : : : | 457 AFSEELTRSTHCPSNNVISERNS 479 324 ALSED----SAPTNDTAANSAS 341 (HUMA-) HUMAN GENOME SCI INC 95WO-US01992. 95WO-US01992. (first entry) WPI; 1996-393343/39. N-PSDB; AAT36375. 178 FNFA-----Rosen CA; Homo sapiens. WO9625432-A1 17-FEB-1995; 17-FEB-1995; 08-DEC-1996 22-AUG-1996. Li Y, 28 55 118 191 219 7 184 AAW0215 ò g QΥ g ŏ g ò g δ a á g δλ g δ g

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Claim 1; Page 45-48; 63pp; English.

XX
XX
XX
CC
This sequence of a human G-protein coupled receptor may be expressed in a host cell using a vector, for production of the recombinant consists of this G-protein coupled receptor (GPCR) can be used to inhibit GPCR, to treat conditions relating to over-expression of the receptor, e.g. asthma, SLE, transplant consistinulate GPCR, to treat conditions relating to under-expression of the receptor, e.g. asthma, SLE, transplant consistinulate GPCR, to treat conditions relating to under-expression of the receptor, e.g. immunodeficiency and severe infections, and consists of bacteril and viral infections, and CSa (mmunoregulatory effect stimulation.

XX
Squence 482 AA;
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11; FIALDRCICVLHPVWAQNHRTVSLAMKVIVGPWILALVLTLPVFLFLTTVTIPNGDTYCT 177 |:||||: | |:| |||| | :| |: ||: ||: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: | 174 YKFGLSSSLDYPDFYGDPLENRSLENIVQPPGEMNDRLDPSSFQINDHPWTVPIVFQPQT 233 219 ICYGLIAAKIHKKGMIKS-SRPLRVLTAVVASFFICWFPFQLVALLGTVWLKEMLFYGKY 277 278 KIIDILVNPTS-------SLAFFNSCLNPMLYVFVGQDFRERLIHSLPTSLER 323 TVTTICYLNLALADFSFTATLPFLIVSMAMGEKWPFGWFLCKLIHIVVDINLFGSVFLIG 117 234 FORPSADSLPRGSARLTSQNLYSNVFKPADVVSPKIPSGFPIEDHETSPLDNSDAFLSTH 293 -------AITMLTARGIIRFVIGFSLPMSIVA 218 Gaps 2 ETN----FSTPLNEYEEVSYESAGYTVLRILPLVVLGVTFVLGVLGNGLVIWVAGFRMTR 57 Query Match
28.0%; Score 508.5; DB 17; Length 482;
Best Local Similarity 26.6%; Pred. No. 3.3e-48;
Matches 134; Conservative 59; Mismatches 117; Indels 193; 324 ALSED----SAPTNDTAANSAS 341 | ||: : | AFSEELTRSTHCPSNNVISERNS 479 LKV-----7 55 118 28 178 184 191 457 δ õ a ŏ a ò g ò 셤 δ g ŏ q à à g

Search completed: December 16, 2002, 17:18:09 Job time: 42 secs

OLASIN MINTER TENDES SILL

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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OM protein - protein search, using sw model

December 16, 2002, 17:17:27 ; Search time 20 Seconds (without alignments) . 1687.159 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-944-807-2 1817 1 METNFSTPLNEYEEVSYESA......TNDTAANSASPPAETELQAM 351

Scoring table:

283224 seqs, 96134422 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

283224 Notal number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_73:* 1: pirl:* 2: pir2:* 3: pir3:* 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

			dF			SUMMARIES	
Result No.	1t.	Score	Query	Length	80	£	Description
	г	81		35	1	B42009	FMLP-related recep
	~	1318		S		C42009	
	ო	1249.5	68.8	3 350	7	A42009	pept
	4	1223.5	67.3	35		A46520	N-formyl peptide r
_	'n	1174.5	64.	36		A49542	
_	9	538.5	29.	37		JC5498	
	7	530.5	29.	7		JC5835	anaphylatoxin C3a
	œ	513	28.	35		A37963	complement C5a ana
	6	509.5	28.	48		865766	G protein-coupled
	10	502.5	27.	37		JC5796	probable chemoattr
	11	502	27.	35		JC2492	G protein-coupled
•	12	200	27.	35		S27357	complement C5a ana
1	13	499	27.	35		A55733	G protein-coupled
~	14	457.5	25.	35		A46525	complement C5a ana
	15	430.5		35		JC2134	
	16	427.5		35		JH0621	angiotensin II rec
	17	426.5		35		JC1104	angiotensin II rec
_	18	426.5		36		A53611	interleukin-8 rece
	19	423.5	23.3	35		S15403	н
• •	20	422.5		32		JQ1231	interleukin-8 rece
. •	21	420.5		32		A42656	angiotensin II rec
. •	22	420.5	23.1	35		JQ1516	angiotensin II rec
	23	419.5	23.1	32		A45747	e Y/
٠,٧	24	418.5	ന	35		A48857	Η
. 1	25	418.5	ന	35		139418	angiotensin II rec
. •	56	418	23.0	35		S44425	II
••	27	413.5	22.8	35		G00048	fusin (LESTRA) - c
. •	28	413.5	22.8	35		JC1194	anglotensin II rec
. •	53	412	22.7	10		A30341	oupl

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A;Molecule type: mRNA
A;Residues: 1-351 <MUR>
A;Residues: 1-351 <MUR>
A;Cossidues: 1-351 <MUR
B;Nomura, H; Nielsen, B;W; Matsushima, K.
Int. Immunol. 5, 1239-1249, 1993
A;Title: Molecular cloning of cDNAs encoding a LD78 receptor and putative leukocyte c A;Reference number: 154751; MulD:94092629; PMID:7505609
A;Accession: 154751
A;Status: preliminary; translated from GB/EMBL/DDBJ

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		#44 EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE	88.000.000.11.11.533.00.00.00.00.00.00.00.00.00.00.00.00.0	3 9 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	000000000000000	UN0694 151372 a a A46226 A46821 155517 b m 533508 542096 A57752 m m A57510 m m A374195 A41795 A41795 A41795 A32297 m m 5332297 m m 5332297 m m 5332297 m m	anglotensin II rec anglotensin II rec somatostatin recep interleukin.8 recep probable G protein interleukin.8 rece mu opioid receptor interleukin.8 rece an opioid receptor interleukin.8 rece somatostatin recep
	RESULT B42009 FMLP-re- N, Alter C; Date: C; Date: C; Acces:	RESULT 1 B42009 FMLP related receptor 1 N.Alternate names: FMLP C.Species: Homo sapiens C.Date: 30-Sep-1993 #sec C.Accession: B42009; JC R.BBO. L.; Gerard, N.P.	ceptor 1 es: FMLP sapiens 1993 #se 2009; JC	1 - human P recepto s (man) equence_r c1258; JQ	tor tor Joil		de receptor like-1; probab nnge 21-Jul-2000 1, C.
*	ATTITLE: Mapping of genes for t. A. Reference number: A42009; MUII A. A. Accession: B42009 A. Status: nucleic acid sequence A. Molecule type: DNA A. Residues: 1.263, A. 265-338, A. Cross-references: GB:N76672 A. Note: authors translated the	verionizes 1.5, 4.3.7.440, 1.95. A;Title: Mapping of genes for the hi A;Teterence number: A42009; MUID:92: A;Accession: B42009 A;Status: nucleic acid sequence not A;Molecule type: DNA A;Residues: 1-263, /A, 265-338, /C, 34 A;Notes references: GB:M76672 A;Note: authors translated the codor	/ 440, g of ger ber: A4; 2009 ic acid : DNA 63, 'A',; ces: GB;	J, 1992 genes for the A42009; WUID:: cld sequence nc A, 265-338,'C', A',265-338,'C', nslated the coc	Tth GID ICe 1	uman C5a receptor (C5AR), 107681; PMID:1612600 shown 10-351 <bao> 18 GTG for residue 15 as</bao>	. human FMLP receptor (FPR Glu, TCT for residue 19 a
*	R; Perez, Gene 118, A; Title: A; Referen A; Accessi A; Molecul A; Residue A; Cross:	R; Perez, H.D.; Holmes, Gene 118, 303-304, 1993 ArTitle: Cloning of a CA; Reference number: JC125 A; Accession: JC125 A; Setus: nucleic acid A; Molecule type: MRNA A; Residues: 1351 CPER>A; Creatences: EMENA A; Control of the contr	H.D.; Holmes, R.; 303-304, 1992 Cloning of a cDNA ce number: JC1258 Lon: JC1258 Lon: JC1258 Letype: mRNA etype: mRNA ss: 1-351 <per></per>	R.; Kelly 2 2 2DNA encoc 1258; MUII sequence 3 3 3 3 5 5 5 5 5 5 7 8 5 7 8 7 8 8 8 8 8 8 8 8	wording, words and words a	E.; McClary, J.; Andrews g a receptor related to 2380523; PMID:1511907 t shown	rmyl peptide recepto
*	A Experi R, Ye, R Hochem A, Title A, Refer A, Molece A, Resid A, Cross	ALEXPELIMENTAL SOURCE: DOTE MAINTON MINNS (R.Ye. R.D.; Cavanagh, S.L.; Quenberge Blochem. Biophys. Res. Commun. 184, 582 A;Title: Isolation of a cDNA that encod A; Reference number: JQ1521; MUID:922469 A; Accession: JQ1521 A;Molecule type: MRNA A;Residues: 1-351 < YE2> A;Cross references: GB:M88107; NID:q189	source: anagh, S anagh, S s. Res. (ton of a ber: JQ1 1521 mRNA 51 <ye2></ye2>	S.L.; C Commun a cDNA 1521; M	tha.	Ajexperimental source: Done marrow mar. RY Fet, R. D.; Cavanaqh, S. L.; Quehanberger, O.; Prossnitz, E.R. Blochem. Biophys. Res. Commun. 184, 582-589, 1992 A. Title: Isolation of a cDNA that encodes a novel granulocyte A. Reference number: JQ1521; MUID:92246937; PMID:1374236 A. Accession: JQ1521 A. Molecule type: mRNA A. Residues: 1-351 CYE2> A. Accessions: GB:M88107; NID:9189862; PID:9189863	R.; Cochrane, C.G.
A	A; Experimen A; Note: for R; Murphy, P T; Biol. Ch A; Title: A A; Reference A; Accession A; Molecule	formyl peptil formyl peptil y, P.M.; Ozce. Chem. 267, . A structura. ence number: ison: Asion: A42492	tal source: grammyl peptide-st. M.; Oxcellk, em. 267, 7637, structural hor in number: A424; i: A42492	granuloc -stimulat k, T.; Ke 37-7643, homologue 2492; MUI	ocy keni v 1	n com .L.; de re 34	comparable to that of the form; McDermott, D.; Francke, U. receptor. Characterization an

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C;Superfamily: vertebrate rhodopsin
C;Keywords: chemotaxis; G protein-coupled receptor; glycoprotein;
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                                                                                                         Query Match 72.5
Best Local Similarity 71.7
Matches 253; Conservative
                                                                                                                                                                                                                                                                                                                                                                                              61
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C;Superfamily: vertebrate rhodopsin
C;Superfamily: vertebrate rhodopsin
C;Superfamily: vertebrate protein-coupled receptor; glycoprotein; transmembrane protein
F;27-53/Domain: transmembrane #status predicted <TM1>
F;59-63/Domain: transmembrane #status predicted <TM2>
F;100-121/Domain: transmembrane #status predicted <TM3>
F;145-169/Domain: transmembrane #status predicted <TM3>
F;206-226/Domain: transmembrane #status predicted <TM3>
F;206-226/Domain:
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u
                                                             A;Cross-references: GB:D10922; NID:g219864; PIDN:BAA01720.1; PID:g219865
C;Comment: This G-protein coupled receptor, homologous to the N-formyl peptide receptor
differentiated myeloid cells and is probably a chemotactic receptor for some other ligar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Bao, L.; Gerard, N.P.; Eddy Jr., R.L.; Shows, T.B.; Gerard, C.
Benomics 13, 437-440, 1992
A;Title: Mapping of genes for the human C5a receptor (C5AR), human FMLP receptor (FPR),
A;Reference number: A42009; MUID:92307681; PMID:1612600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:M76673; NID:9182668; PID:9182669
C;Comment: This fMet-Leu-Phe receptor homolog, whose ligand is not yet known, appears
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FMLP-related receptor 2 - human N;Alternate names: FMLP-related receptor I; probable chemotactic receptor FPRH2 C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Date:: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 26-Aug-1999 C;Accession: C42009
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ASWGGTPEERLKVAITMLTARGIIRFVIGFSLPMSIVAICYGLIAAKIHKKGMIKSSRPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F:242-266/Pomain: transmembrane #status predicted <TM6>
F:282-307/Domain: transmembrane #status predicted <TM7>
4/Binding site: carbohydrate (Asn) (covalent) #status predicted
98-176/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LYVFVGQDFRERLIHSLPTSLERALSEDSAPTNDTAANSASPPAETELQAM 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
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Pred. No. 3.3e-145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%; Score 1817; Best Local Similarity 100.0%; Pred. No. 3.3 Matches 351; Conservative 0; Mismatches
                                                                                                                                                                                                                                                OMIM: 136538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Gene: GDB:FPRL2
A;Cross-references: GDB:128855; OMIM:136539
A;Map position: 19q13.3-19q13.4
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                                                                                                                                                                                                                                            A; Cross-references: GDB:127554;
A; Map position: 19q13.3-19q13.4
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                                -351 <RES>
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                                                                                                                                                                                                        A; Gene: GDB: FPRL1
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A; Westerence number: JC2014; MUID:94040825; PMID:8224916
A; Accession: JC2014
A; Wolecule type: mRNA
A; Wolecule type: mRNA
A; Wolecule type: mRNA
A; Wolecule type: mRNA
A; Wote: 1929-48n was also found
A; Title: The human N-formylpeptide receptor: Characterization of two CDNA isolates an A; Reboulay; F:; Tardif, M.; Brouchon, L.; Vignais, P.
Biochemistry 29, 11123-11133, 1990
A; Fittle: The human N-formylpeptide receptor: Characterization of two CDNA isolates an A; Reference number: A3309; MUID:9105045; PMID:2176894
A; Reference number: A3309; MUID:9105045; PMID:2176894
A; Reference number: A3509; MUID:9105045; PMID:2176894
A; Residues: 1-191, N', 193-345, E', 347-350 cBOUJ>
A; Residues: 1-191, N', 193-345, E', 347-350 cBOUJ>
A; Cross-references: GB:MGOGZ; GB:M33538; NID:9182664; PIDN:AAA35847.1; PID:9182665
B; Boulay, F:; Tardif, M.; Brouchon, L.; Vignais, P.
B; Boulay, F:; Tardif, M.; Brouchon, L.; Vignais, P.
B; Boulay, F:; Tardif, M.; Brouchon, L.; Vignais, P.
B; Rochem: Biophys: Res. Commun. 168, 110-1109, 1990
A; Title: Synthesis and use of a novel N-formyl peptide derivative to isolate a human A; Reference number: A35495; MUID:920507449; PMID:2161213
A; Molecule type: mRNA
A; Residues: 1-100, L', 102-191, N', 193-350 cBOUZ>
A; Molecule type: mRNA
A; Residues: 1-100, L', 102-191, N', 193-350 cBOUZ>
A; Title: Mapping of genes for the human C5a receptor (C5AR), human FMLP receptor (FPR A; Reference number: A42009; MUID:92307681; PMID:1612600
A; Recence number: A42009; MUID:92307681; PMID:1612600
A; Recence number: A42009; MUID:92307681; PMID:1612600
A; Receptor type: DNA
   prote
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transmembrane
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C;Species: Homo sapiens (man)
C;bate: 30-Sep-1993 #sequence_revision 14-Jul-1995 #text_change 24-Nov-1999
C;Accession: JC2014, A36309; A35495; A42009; I52414
G*Murphy, P.M.; Tiffany, H.L.; McDermott, D.; Ahuja, S.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RVLTAVVASFFICWFPFQLVALLGTVWLKEMLFYGKYKIIDILVNPTSSLAFFNSCLNPM 300
                                                                                                                                                                                                                                                      1 METNESTPLNEYEEVSTESAGYTVLRILPLVVLGVTFVLGVLGNGLVIWVAGFRMTRTVT 60
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                                                                    Length 353;
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                                                            72.5%; Score 1318; DB 2; 71.7%; Pred. No. 2.8e-103; ive 39; Mismatches 59;
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67.3%;
ilarity 67.7%;
Conservative 41
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Best Local Similarity 64.69
Matches 237; Conservative
                                                                                                                            Similarity
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A; Residues: 1-364 <GAO>
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                                                                                                   Query Match
Best Local Simil
Matches 239; (
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A; Residues: 1, 'G',3-28,30-100, 'L',102-104,106-112,'FLIA',115-176,178-182,184-191,'N',194
R; Perez, H.D.; Holmes, R.; Kelly, E.; McClary, J.; Chou, Q.; Andrews, W.H.
Bochemistry 31, 11595-11599, 1992
A;Title: Cloning of the gene coding for a human receptor for formyl peptides. Characteri
A;Reference number: 152414; MUID:93075765; PMID:1445895
                                                                                                                                                                                                                                                                                 A. Cross references: GDB:127999; OMIM:136537
A. Map position: 19q13.4-19q13.4
A. Map position: 19q13.4-19q13.4
A. Map position: 19q13.4-19q13.4
A. Map position: #status absent
A. Map position: glycoretion is found in exon 3; alternatively spliced mRNA transcripts
C. Superfamily: vertebrate rhodopsin
F. 27-53/Domain: transmembrane #status predicted <TM2>
A. Tolonalin: transmembrane #status predicted <TM3>
A. Tolonalin: transmembrane #status predicted <TM3>
A. Tolonalin: transmembrane #status predicted <TM3>
F. 242-266/Domain: transmembrane #status predicted <TM5>
F. 242-266/Domain: transmembrane #status predicted <TM5>
F. 242-266/Domain: transmembrane #status predicted <TM5>
F. 379-304/Domain: transmembrane #status predicted <TM7>
F. 4. 10/Binding site: carbohydrate (Asn) (covalent) #status predicted
F. 39-176/Disulfide bonds: #status predicted
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C;Species: Oryccolagus cuniculus (domestic rabbit)
C;Dacte: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C;Accession: A46520
R;Ye, R.D.; Quehenberger, O.; Thomas, K.M.; Navarro, J.; Cavanagh, S.L.; Prossnitz,
J. Immunol. 150, 1383-1394, 1993
A;Title: The rabbit neutrophil N-formyl peptide receptor. cDNA cloning, expression,
A;Reference number: A46520; MUID:93163563; PMID:8432984
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 ASWGGTPEERLKVAITMLTARGIIRFVIGFSLPMSIVAICYGLIAAKIHKKGMIKSSRPL 240
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A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Status: preliminary
A; Residues: 1-5 < PER>
A; Cross-references: GB: S49810; NID: 9260832; PIDN: AAD14906.1; PID: 94262758
A; Genetics:
A; Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 1249.5; DB 2; Length
Pred. No. 1.6e-97;
37; Mismatches 71; Indels
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Best Local S
Matches 241
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Formyl peptide chemotactic receptor - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change 05-Nov-1999
C;Accession: A49542
J. Biol. Chem. 268, 25395-25401, 1993
A;Title: Species and subtype variants of the N-formyl peptide chemotactic receptor re
A;Reference number: A49542; MUID:940646602; PMID:8244972
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PLRVLTAVVASFFICWFPFQLVALLGTVWLKEMLFYGKYKIIDILVNPTSSLAFFNSCLN 298
                                                                                                                                                                                                                                                                                                                 61 TICYLNLALADFSFTATLPFLIVSMAMGEKWPFGWFLCKLIHIVVDINLFGSVFLIGFIA 120
                                                                                                                                                                                                                                                                                                                                                                                                                     LDRCICVLHPVWAQNHRTVSLAMKVIVGPWILALVLTLPVFLFLTTVTIPN--GDTYCTF 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----GDTYCTFNFASWGGTPEERLKVAITMLTARGIIRFVIGFSLPMSIVAICYGLIAAK 227
                                                                                                                                                         Gaps
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                                                                                                                                                                                                          1 METNFSTPLNEYEEVSYESAGYTVLRILPLVVLGVTFVLGVLGVLGVLWVAGFRMTRTVT 60
                                                                                                                                                                                                                                        1 METNFSTPLNEYE-----EVSYESAGYTVLRILPLVVLGVTFVLGVLGNGLVIWVAG 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Cross-references: GB: L22181; NID: 9347396; PIDN: AAA16110.1; PID: 9347397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 364;
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                                                                                                         Length
A;Note: sequence extracted from NCBI backbone (NCBIP:124908)
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; transmembrane protein
                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2;
                                                                                                            .;
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                                                                                                      Score 1223.5; DB 2;
Pred. No. 2.4e-95;
41; Mismatches 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64.6%; Score 1174.5; DB 2; 64.6%; Pred. No. 3.3e-91; ive 38; Mismatches 73;
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C;Superfamily: vertebrate rhodopsin
C;Keywords: chemotaxis; transmembrane protein
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Matches 133; Conservative
                                                                                                                                                                                                                                                                                                                         Similarity
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Cochem. Biophys. Res. Commun. 233, 336-342, 1997
Aritle: A novel G protein-coupled receptor with homology to neuropeptide and chemoattra
A; Reference number: JC5498; MUID:97289630; PMID:9144535
A; Contents: Brain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            anaphylatoxin C3a receptor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 05-Mar-1998 #sequence_revision 13-Mar-1998 #text_change 17-Mar-2000
C;Accession: JC5835
R;Fukuoka, Y.; Ember, J.A.; Hugli, T.E.
Biochem. Biophys. Res. Commun. 242, 663-668, 1998
A;Title: Cloning and characterization of rat C3a receptor: Differential expression of A;Reference number: JC5835; MUID:98125550; PMID:9464274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
                                                                                                                                                                                                                                                                                                      Species: Mus musculus (house mouse)

Date: 07-Jul-1997 #sequence_revision 29-Aug-1997 #text_change 19-May-2000

Accession: JC5498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:U79525; NID:g1732346; PIDN:AAB53789.1; PID:g1732347
C;Comment: This protein is involved in the bone metabolism.
C;Superfamily: vertebrate rhodopsin
F;110-187/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     298 SPLAFFNSCLNPMLYVFWGQDFRERLIHSLPASLERALTEDSAQTSDTGTNLGTNSTSLS 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 ICYLNLALADFSFTATLPFLIVSMAMGEKWPFGWFLCKLIHIVVDINLFGSVFLIGFIAL 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                74 VWFVNLAVADFLENIFLPMHITYAAMDYHWVFGKAMCKISNFLLSHNMYTSVFLLTVISF 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     122 DRCICVLHPVWAQNHRTVSLAMKVIVGPWILALVLTLPVFLFLTTVTIPNGDTYCTFNFA 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           182 SWGGTPEERLKVAITMLTARG-----IIRFVIGFSLPMSIVAICYGLIAAKIHKKGM 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      234 IKSSRPLRVLTAVVASFFICWFPFQLVALLGTVWLKEMLFYGKYKIIDILVNP-TSSLAF 292
                                                                          SSLAFFNSCLNPMLYVFVGQDFRERLIHSLPTSLERALSEDSAPTNDTAAN---SASPPA 344
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 371;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29.6%; Score 538.5; DB 2; Length 37
35.2%; Pred. No. 9.3e-38;
tive 70; Mismatches 124; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      293 FNSCLNPMLYVFVGQDFRERLIHSLPTSLERALSEDSAPTN 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 29.6%
Best Local Similarity 35.2%
Matches 120; Conservative
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                                                                                                                                                                                                                                                                                    protein-coupled receptor
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A; Molecule type: mRNA
A; Residues: 1-371 <MET>
                                                                                                                                                                              358 ENTLNAM 364
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A.Cross references: GB:U86379; NID:g3015534; PIDN:AAC40071.1; PID:g2853279
A.Experimental source: brain
C.Comment: This receptor plays a role in the central nervous systems.
C.Comment: This receptor plays a role in the central nervous systems.
C.Superfamily: vertebrate rhodopsin
C.Superfamily: vertebrate rhodopsin
C.Steywords: glycoprotein; phosphoprotein
C.Steywords: glycoprotein; pransmembrane #status predicted <TM3>
F.25-51/Domain: transmembrane #status predicted <TM3>
F.36-33/Domain: transmembrane #status predicted <TM4>
F.32-347/Domain: transmembrane #status predicted <TM5>
F.36-39/Domain: transmembrane #status predicted <TM5>
F.36-39/Domain: transmembrane #status predicted <TM5>
F.36-39/Domain: transmembrane #status predicted <TM5>
F.36-30/Domain: transmembrane #status predicted <T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2; Length 473;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29.2%; Score 530.5; DB 2; Length 4 28.9%; Pred. No. 5.7e-37; ive 60; Mismatches 107; Indels
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G protein-coupled receptor (clone A23B) - human
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 21-Jul-2000
C; Accession: S65766
E; Royaltc, A.; Prossnitz, E.R.; Cavanagh, S.L.; Pan, Z.; Zou, A.; Ye, R.D.
Biochim. Blophys. Acta 1305, 39-43, 1996
A; Title: cDNA cloning of a novel G protein-coupled receptor with a large extracellula A; Reference number: S65766; MUID:96180983; PMID:8605247
A; Ratus: preliminary
A; Molecule type: mRNA
A; Ratus: preliminary
A; Molecule type: mRNA
A; References: EMBL: C128488; NID:91199577; PIDN: AAC50374.1; PID:91199578
C; Superfamily: vertebrate rhodopsin
C; Keywords: G protein-coupled receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     encoding a novel chemoattr
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A;Reaidues: 1-371 <0NMA.
A;Crosa-teferences: DDBJ:AJ002745; NID:g2624397; PIDN:CAA05715.1; PID:g2624398
A;Experimental source: 11ver
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58 TVTTICYLNLALADFSFTATLPFLIVSMAMGEKWPFGWFLCKLIHIVVDINLFGSVFLIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             118 FIALDRCICVLHPVWAQNHRTVSLAMKVIVGPWILALVLTLPVFLFLTTVTIPNGDTYCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    174 YKFGLSSSLDYPDFYGDPLENRSLENIVQRPGEMNDRLDPSSFOTNDHPWTVPTVFQPQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       234 FQRPSADSLPRGSARLTSQNLYSNVFKPADVVSPKIPSGFPIEDHETSPLDNSDAFLSTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KIIDILVNPTS-----SLAFFNSCLNPMLYVFVGQDFRERLIHSLPTSLER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels 193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 482;
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C; Species: Rattus norvegicus (Norway rat)
C; Date: 24-Jan-1998 #sequence_revision 13-Mar-1998 #tex
C; Accession: JC5796
R; Wwman, C.; Lolait, S.J.; Santen, S.; Olde, B.
B; Accession: Biophys. Res. Commun. 241, 390-394, 1997
A; Title: Molecular cloning and tissue distribution of cl
A; Reference number: JC5796; MuID:98086361; PMID:9425281
                                                                                                                                                                                                                                                                                                                                                                                                                                            28.0%; Score 509.5; DB 2; 26.6%; Pred. No. 3.4e-35; ive 59; Mismatches 117;
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Best Local Similarity 26.6%
Matches 134; Conservative
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                                           Rigerard, N.P.; Bao, L.; Alao-Ping, H.; Eddy, R.L.
Biochemistry 32, 1243-1250, 1993
A; Title: Human chemotaxis receptor genes cluster at 19q13.3-13.4. Characterization of th A; Reference number: 152417; MUID:93192225; PMID:838326
A; Recession: 152417; MUID:93192225; PMID:838326
A; Accession: 152417; MUID:93192225; PMID:838326
A; Accession: 152417; MUID:93192225; PMID:838356
A; Accession: 152417; MUID:93192225; PMID:838356
A; Accession: 152417; MUID:9319225; PMID:9298577; NID:9298578
A; Cross-references: GB:55556; GB:55557; NID:9298577; NID:9298578
A; Cross-references: GB:128856; OMIM:113995
A; Map position: 19q13.3-19q13.4
A; Introns: 1/3
A; Introns: 1/3
A; Docte: the list of introns may be incomplete
C; Function: mediates the inflammatory and chemotactic responses of polymorphonuclear no s; Superfamily: vertebrate rhodopsin
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Keywords: chemotaxis; G protein-coupled receptor; glycoprotein; inflammation; polymorp
F:1-37/Domain: extracellular #status predicted <EX1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          polymorphonuclear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   114 FLIGFIALDRCICVLHPVWAQNHRTVSLAMKVIVGPWILALVLTLPVFLFLTTVTIPNGD 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           229 TWSRRATRSTKTLKVVVAVVASFFIFWLPYQVTGIM-----MSFLEPSSPTFLLLNKL 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            174 TY-----CTFNFASWGGTPEERLKVAITMLTARGIIRFVIGFSLPMSIVAICYGLIAAK 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IHKKGMIKSSRPLRVLTAVVASFFICWFPFQLVALLGTVWLKEMLFYGKYKIIDILVNPT 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SSL----AFFNSCLNPMLYVFVGQDFRERLIHSLPTSLERALSEDSA------PTND 334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         180 EYFPFKVLCGVDYSH-----DKRRERAV-----AIVRLVLGFLWPLLTLTLTCTFLILR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F)62-71/Domain: intracellular #status predicted <IN1>
F)72-94/Domain: transmembrane #status predicted <IN1>
F)72-94/Domain: extracellular #status predicted <EX2>
F)711-132/Domain: transmembrane #status predicted <EX2>
F)111-132/Domain: transmembrane #status predicted <IN3>
F)13-149/Domain: intracellular #status predicted <IN2>
F)150-174/Domain: extracellular #status predicted <IN3>
F)20-227/Domain: extracellular #status predicted <FM5>
F)228-242/Domain: transmembrane #status predicted <IN3>
F)243-264/Domain: transmembrane #status predicted <IN5>
F)265-283/Domain: extracellular #status predicted <IM6>
F)265-283/Domain: intracellular #status predicted <IM7>
F)308-350/Domain: intracellular #status predicted <IM7>
F)308-350/Domain: intracellular #status predicted <IM7>
F)5/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 350;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28.2%; Score 513; DB 1; Length 35
33.6%; Pred. No. 1.2e-35;
iive 60; Mismatches 129; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F:38-61/Domain: transmembrane #status predicted <TM1>F:62-71/Domain: intracellular #status predicted <IN1>
                             Cross-references: EMBL:X58674; NID:g29568;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best_Local Similarity 33.6
Matches 122; Conservative
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DRCICVLHPVWAQNHRTVSLAMKVIVGPWILALVLTLPVFLFLTTVTIPNGDTYCTFNFA 181
                                                                                                                                                                                                                                    ICYLNLALADFSFTATLPFLIVSMAMGEKWPFGWFLCKLIHIVVDINLFGSVFLIGFIAL
                                                                                                                                                                                                                                                                                                       SWGGTPEERLKVAITMLTARGI - - IRFVIGFSLPMSIVAICYGLIAAKIHKKGMIKSSRP
                                                                                                                                                                                                                                                                                                                                    : : | : : | | : : | | EX------ELTLARHHVLTWVKFLFGYLLPLLTMSSCYLCLIFKTKKQNILISSKH
       NFSTPLNEY-EEVSYESAGYT-VLRILPLVVLGVTFVLGVLGNGLVIWVAGFRMTRTVTT
                                                      14 NYSYALEYYSOEPDAEENVYPGIVHWISLLLYALAFVLGIPGNAIVIWFMGFKWKKTVTT
                                                                                                                                                                                                                                                                                                                                                                                                      240 LRVLTAVVASFFICWFPFQLVALLGTVWLKEMLFYGKYKIIDIL---VNPTSSLAFFNSC
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LNPILYVIISKKFQARFRASVAEVLKRSLWEAS 329
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Matches 113;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N'Alternate names: GPR-1
C:Species: Rattus norregicus (Norway rat)
C:Species: Rattus norregicus (Norway rat)
Accession: JC2492
Marchese, A.; Cheng, R.; Lee, M.C.; Porter, C.A.; Heiber, M.; Goodman, M.; George, S.F.
Jochem. Blophys. Res. Commun. 205, 1952-1958, 1994 receptor genes: An amino acid different A:Reference number: JC2492; MJID:95110347; PMID:7811287
A:Reference number: JC2492; MJID:95110347; PMID:7811287
A:Residues: 1-353 CAMPA
A:Residues: 1-353 CAMPA
A:Residues: 1-353 CAMPA
A:Residues: JC2492; MJID:9786483; PIDN:AAB32978:1; PID:9786484
C:Superfamily: vertebrate rhodopsin
C:Superfamily: vertebrate rhodopsin
     cha
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F:150,231/Binding site: phosphate (Thr) (covalent) (by protein kinase A) #status predict
F:330/Binding site: palmitate (Cys) (covalent) #status predicted
     during a microbial
                                                                                                                                                                                                                                                                                                                                                        6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RCICVLHPVWAQNHRTVSLAMKVIVGPWILALVLTLPVFLFLTTVTIPNGDTYCTFNFAS 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 246 QRNRQAKTKKPPKIIITIIITFFLCWCPYH-----TLYLLELHHTAVPASVFSLGLPLA 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63 CYLNLALADFSFTATLPFLIVSMAMGEKWPFGWFLCKLIHIVVDINLFGSVFLIGFIALD 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                 11 EYEE-----VSYESAG---YTVLRILPLVVLGVTFVLGVLGNGLVIWVAGFRMTRTVTTI 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---RLKVAITMLTARGIIRFVIGFSLPMSIVAICYGLIAAKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HKKGMIKSSRPLRVLTAVVASFFICWFPFQLVALLGTVWLKEMLFYGKYKIIDILVNP-T
                                                                                                                      F)112-135/Domain: transmembrane #status predicted <TM3>
F)156-177/Domain: transmembrane #status predicted <TM4>
F)206-237/Domain: transmembrane #status predicted <TM5>
F)205-280/Domain: transmembrane #status predicted <TM5>
F)302-317/Domain: transmembrane #status predicted <TM7>
F)302-317/Domain: transmembrane #status predicted <TM7>
F)7/190/Binding site: carbohydrate (Asn) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                     27.7%; Score 502.5; DB 2; Length 371; 34.7%; Pred. No. 9.9e-35;
     cells
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300 TAVAIANSCMNPILYVFMGHDFKKFKV-ALFSRLVNALSEDTGPSS 344
protein regulates the trafficking of immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SSLAFFNSCLNPMLYVFVGQDFRERLIHSLPTSLERALSEDSAPTN 333
                         C;Superfamily: vertebrate rhodopsin
C;Keywords: glycoprotein; receptor; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;209-229/Domain: transmembrane #status predicted <TM5>F;246-266/Domain: transmembrane #status predicted <TM6>F;295-306/Domain: transmembrane #status predicted <TM7>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F;112-133/{\rm Domain}: transmembrane #status predicted <TM3> F;134-135/{\rm Region}: DR motif
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                                                                                                                                                                                                                                                                                                                                                      Mismatches 124;
                                                                        F)39-62/Domain: transmembrane #status predicted <Fm1> F)74-94/Domain: transmembrane #status predicted <Fm2>
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                                                                                                                                                                                                                                                                                                                                                   63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein-coupled receptor 1 - rat
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Matches 120;
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Best Local S
Matches 114
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A; Accession: 24.7337
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A; Residues: 1-352 <-PER>
A; Residues: 1-352 <-PER>
A; Residues: 1-352 <-PER>
A; Residues: 1-352 <-PER>
A; Cross-references: EMBL:X65860; NID:9878; PIDN:CAA46690.1; PID:9879
C; Function:
A; Description: mediates the inflammatory and chemotactic responses of polymorphonucle of Keywords: chemotaxis; G protein-coupled receptor; glycoprotein; inflammation; polym C; Reywords: chemotaxis; G protein-coupled receptor; glycoprotein; inflammation; polym F; 1-39 formain: extracellular #status predicted <rp>F; 63-72 /Domain: transmembrane #status predicted <rp>F; 73-95 /Domain: extracellular #status predicted <rp>F; 73-95 /Domain: extracellular #status predicted 
F; 73-95 /Domain: transmembrane #status predicted 
F; 712-133 /Domain: transmembrane #status predicted 
F; 712-135 /Domain: intracellular #status predicted 
F; 7209-229 /Domain: transmembrane #status predicted 
F; 7207-286 /Domain: transmembrane #status predicted 
F; 7207-286 /Domain: intracellular #status predicted 
F; 245-266 /Domain: transmembrane #status predicted 
                                                                                                                                                                                                                                                                                        of the canine anaphylatoxin C5a receptor PMID:1472004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7;
                                        C;Species: Canis lupus familiaris (dog)
C;Accession: 527357; MUD: 992
R;Perret, J.J.; Raspe, E.; Vassart, G.; Parmentier, M.
Biochem. J. 288, 911-917, 1992
A;Title: Cloning and functional expression of the canine anaphylatoxin C5a 1A;Reference number: $27357; MUID: 93111969; PMID: 1472004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53 FRWTRTVTTICYLNLALADFSFTATLPFLIVSMAMGEKWPFGWFLCKLIHIVVDINLFGS 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 352;
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complement C5a anaphylatoxin receptor - dog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      q
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Keywords: chemotaxis; G protein-coupled receptor; glycoprotein; inflammation; polym:1-37/Domain: extracellular #status predicted <EX1>
38-61/Domain: transmembrane #status predicted <TM1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Description: mediates the inflammatory and chemotactic responses of polymorphonucle
                                                                                                                                                                                                                                of peptidergic G-protein-cou
                                                                                                                                                                                                                                                                                                                                                                            A:Residues: 1.751 <GER>
A:Residues: 3251 <GER>
A:Cross-references: GB:S46665; GB:L05630; NID:g257519; PIDN:AAB97774.1; PID:g257520
A:Experimental source: BALB/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                              Dmplement C5a anaphylatoxin receptor - mouse
Species: Mus musculus (house mouse)
Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    87 MGEKWPFGWFLCKLIHIVVDINLFGSVFLIGFIALDRCICVLHPVWAQNHRTVSLAMKVI 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   206 FVIGFSLPMSIVAICYGLIAAKIHKKGMIKSSRPLRVLTAVVASFFICWFPFQLVALLGT 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27 ILPLVVLGVTFVLGVLGNGLVIWVAGFRMTRTVTTICYLNLALADFSFTATLPFLIVSMA 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : |:: | |::|| || ||:|| || 38 VAALIIYSVVFLVGVPGNALVVWVTAFEPDGPSNAIWFLNLAVADLLSCLAMPVLFTTVL 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            147 VGPWILALVLTLPVFLFLTTV-TIPNGDTYCTFNFASWGGTPEERLKVAITMLTARGIIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VWLKEMLFYGKYKIIDILVNPTSSLAFFNSCLNPMLYVFVGQDFRERLIHSLPTSLERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 351;
                                                                                                                                                               O.; Pearson, M.; Kunz, D.; Gerard,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           predicted
                                                                                                                                                                                                                                                                                                                  A;Status: preliminary; not compared with conceptual translation A;Wolecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C. Superfamily: vertebrate rhodopsin
C. Superfamily: vertebrate rhodopsin
C. Superfamily: vertebrate rhodopsin
C. Superfamily: vertebrate rhodopsin
C. Superfamily: vertebrates rhodopsin
C. Superfamily: vertebrates of protein-coupled receptor; glycop
F.14-37/Domain: extracellular #status predicted <TML>
F. 72-94/Domain: transmembrane #status predicted <TML>
F. 95-110/Domain: extracellular #status predicted <TML>
F. 95-110/Domain: extracellular #status predicted <TML>
F. 111-122/Domain: intracellular #status predicted <TML>
F. 133-149/Domain: extracellular #status predicted <TML>
F. 150-174/Domain: extracellular #status predicted <TML>
F. 150-228/Domain: intracellular #status predicted <TML>
F. 244-56/Domain: intracellular #status predicted <TML>
F. 244-66/Domain: intracellular #status predicted <TML>
F. 
                                                                                                                                                                                                                      A; Title: Structural diversity in the extracellular faces A; Reference number: A46525; MUID:93017861; PMID:1401897 A; Accession: A46525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           carbohydrate (Asn) (covalent) #status
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31.8%; Pred. No. 5.6e-31;
11ve 62; Mismatches 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;285-308/Domain: transmembrane *status predicted F;309-351/Domain: intracellular *status predicted
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N'Alternate names: ATIa receptor; AT3 recc
C;Species: Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  326 SEDSA-----PINDIAANSA 340
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                                                                                                                                                         R;Gerard, C.; Bao, L.; Orozco, O. J. Immunol. 149, 2600-2606, 1992
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Best Local Similarity 31.83
Matches 103; Conservative
                                                                                                                                 C; Accession: A46525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6/Binding site:
                                     complement
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Grotein-coupled receptor GPRI - human
C; Species: Homo sapiens (man)
C; Accession: A55733
R; Marchese, A.; Docherty, J.M.; Nguyen, T.; Heiber, M.; Cheng, R.; Heng, H.H.Q.;
Genomics 23, 609-618, 1994
A; Title: Cloning of human genes encoding novel G protein-coupled receptors.
A; Reference number: A55733; MUID:95154831; PMID:7851889
A; Accession: A55733
A; Status: preliminary
A; Molecule type: DNA
A; Status: Preliminary
A; Molecule type: DNA
A; Residues: 1-355 AMAR>
A; Cross: references: GB:013666; NID:9577412; PIDN:AAA64592.1; PID:9577413
C; Genetics:
A; Gene: GDB:371707; OMIM: 600239
A; Map position: 15q25-15q26.1
C; Superfamily: vertebrate rhodopsin
C; Keywords: G protein-coupled receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7;
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289 AVAXINCCINPIIYVLAAQGEHSRFLKSLPARLRQVLAEESVGRDSKSITLSTVDTPAQK 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               226
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                                                                                                                                                               185 FWMT-CGVDYSGVG------VLVERGVAILRLIMGFLGPLVILSICYTFLLIRT 231
                                                                                                                                                                                                                                                           229 HKKGMIKSSRPLRVLTAVVASFFICWFPFQLVALLGTVWLKEMLFYGKYKIIDILVNPTS 288
                                                                                                                                                                                                                                                                                                                                                                                      SLAFFNSCLNPMLYVFVGQDFRERLIHSLPTSLERALSEDSA-----PTNDTAANS 339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 284
VFLIGFIALDRCICVLHPVWAQNHRTVSLAMKVIVGPWILLALVLTLPVFLF--LTTVTIP 170
                                  WVAGFRMTRTVTTICYLNLALADFSFTATLPFLIVSMAMGEKWPFGWFLCKLIHIVVDIN 108
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Best Local Similarity 33.3%; Pred. No. 1.9e-34;
Matches 115; Conservative 68; Mismatches 132; Indels
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C; Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 24-Nov-1999
C; Accession: JC2134; S15404; S20424; JQ1055
R; Conchon, S.; Monnot, C.; Sirieix, M.E.; Bihoreau, C.; Corvol, P.; Clauser, E.
Biochem. Biophys. Res. Commun. 199, 1347-1354, 1994
A; Title: Synthetic cDNA encoding the rat Airla receptor: a useful tool for structure-func
A; Reference number: JC2134; MUID:94197726; PMID:8147879
A; Rocession: JC2134; MUID:94197726; PMID:8147879
A; Rocession: JC2134
A; Molecule type: mRNA
A; Residues: 1-359 <CON>
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A; Reference number: S15404
A; Title: Isolation of a cDNA encoding the vascular type-1 angiotensin II receptor.
A; Reference number: S15404
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-359 <MUR>
A; Cross-references: GB:X62295; NID:957773; PIDN:CAA44183.1; PID:957774
Iwal, N.; Inagami, T.
Bs Lett. 298, 257-260, 1992
A; Reserve con mumber: S20423; MUID:92183879; PMID:1544458
A; Reserve con mumber: S20423; MUID:92183879; PMID:1544458
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A; Molecule type: mRNA
A; Molecule type: mNNA
A; Molecule type: mNNA
A; Molecule type: multiplication of the gene expression
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Ci Comment: ATI receptor consists of two closely related ATI isoforms of angiotensin II of Comment: ATI receptor consists of two closely related ATI isoforms of angiotensin II of Superfamily: vertebrate rhodopsin

Ci Superfamily: vertebrate rhodopsin

Ci Superfamily: vertebrate rhodopsin

Ci Reywords: G protein-coupled receptor; glycoprotein; GTP binding; receptor; transmembra

Ci St 70 66 Domain: transmembrane #status predicted <TM3>

Fi 103-123 /Domain: transmembrane #status predicted <TM4>

Fi 195-218 /Domain: transmembrane #status predicted <TM5>

Fi 240-263 /Domain: transmembrane #status predicted <TM5>

Fi 240-263 /Domain: transmembrane #status predicted <TM7>

Fi 240-263 /Domain: transmembrane #status predicted <TM7>
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A;Residues: 1-80, C',82-108, T',110-359 <IW2>
A;Cross-references: GB:M74054; NID:9202918; PIDN:AAA40738.1; PID:9202919
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327 HSSLSTKMSTLSYRPSDNMSSSAKKPA 353

Search completed: December 16, 2002, 17:19:57 Job time: 21 secs

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OM protein - protein search, using sw model

December 16, 2002, 17:15:57 ; Search time 14 Seconds (without alignments) 1039.871 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-944-807-2 1817 1 METNESTPLNEYEEVSYESA.....TNDTAANSASPPAETELQAM 351

Scoring table:

112892 seqs, 41476328 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

112892 otal number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

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Burkhart-Schultz K., Gordon L., Dias J., Ramirez M., Stilwagen S.,
Phan H., Velasco N., Do L., Regala W., Terry A., Brower A., Garnes J.,
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Arellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A.,
Olsen A.S., Carrano A.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Aspirin-triggered 15-epi-lipoxin A4 (LXA4) and LXA4 stable analogues are potent inhibitors of acute inflammation: evidence for anti-inflammatory receptors.";

J. EXP. Med. 185:1693-1704 (1997).

-!- FUNCTION: LOW AFFINITY RECEPTOR TO N-FORMYL-METHIONYL PEPTIDES, WHICH ARE POWERFUL NEUTROPHILS CHEMOTACTIC FACTORS. BINDING OF RALP TO THE RECEPTOR CAGUES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A G-PROTEIN THAT ACTIVATES A PHOSPHATIDYLINGSITOL-CALCIUM SECOND MESSENGER SYSTEM: THE ACTIVATION OF LXA4R COULD RESULT IN A NATI-IRFLAMMATORY OUTCOME COUNTERACTING THE ACTIONS OF PROINFLAMMATORY SIGNALS SUCH AS LTB4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCÁTION: Integral membrane protein.
TISSUE SPECIFICITY: EXPRESSED ABUDAWILY IN THE LUNG AND
NEUTROPHILS. ALSO FOUND IN THE SPLEEN AND TESTIS.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPPORS.
                                                                                                                        SEQUENCE FROM N.A.

MEDLINE-20215774; PubMed-9547339;
Gronert F., Gewirtz A., Madara J.L., Serhan C.N.;
Gronert F., Gewirtz A., Madara J.L., Serhan C.N.;
"Identification of a human enterocyte lipoxin A4 receptor that is regulated by interleukin (IL)-13 and interferon gamma and inhibits tumor necrosis factor alpha-induced IL-8 release.";
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                                           Maddox J.F., Hachicha M., Takano T., Petasis N.A., Fokin V.V.,
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Takano T., Flore S., Maddox J.F., Brady H.R., Petasis N.A.,
Serhan C.N.;
                                                                                   Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam, PF00001; 7tm_1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
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EMBL; M84562; AAA52473.1; -...
EMBL; D10922; BAA01720.1; -...
EMBL; U81501; AAB51133.1; -...
EMBL; AF054013; AAC13684.1; -...
EMBL; AC018755; AAF87844.1; -...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M76672; AAA58481.1; -. EMBL; X63819; CAA45319.1; -.
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Genew; HGNC:3827; FPRL1.
MIM; 136538; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JQ1521; JQ1521.
B42009; B42009.
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A42492; A42492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE SPECIFICITY.
[6]
SEQUENCE FROM N.A.
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PIR;
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61 TICYLNLALADFSFTATLPFLIVSMAMGEKWPFGWFLCKLIHIVVDINLFGSVFLIGFIA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RVLTAVVASFFICWFPFQLVALLGTVWLKEMLFYGKYKIIDILVNPTSSLAFFNSCLNPM 300
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                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                non-human primates.";
Immunogenetics 44:446-452(1996).
-!- FUNCTION: LOW AFFINITY RECEPTOR TO N-FORMYL-METHIONYL PEPTIDES,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alvarez V., Coto E., Sehen F., Gouzalek-Koces S., Lopez-Larrea C.; "Molecular evolution of the N-formyl peptide and C5a receptors in
                                                                                                                                                                                                                                                                                                                                         1 METNESTPLNEYEEVSYESAGYTVLRILPLVVLGVTFVLGVLGNGLVIWVAGFRMTRTVT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pan troglodytes (Chimpanzee).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                     N-LINKED (GLCNAC. . .) (POTENTIAL).
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                                                                                                                                                                                                                                                                              DB 1; Length 351;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein;
                                                                     2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                                     EXTRACELLULAR (POTENTIAL).
                                                                                                                      4 (POTENTIAL). EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                    6 (POTENTIAL). EXTRACELLULAR (POTENTIAL).
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DC6AlD77AFC0D780 CRC64;
                                               1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                             3 (POTENTIAL). CYTOPLASMIC (POTENTIAL).
                                                                                                                                           5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                              Score los,,
Pred, No. 1e-97;
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15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FMLP-related receptor I (FMLP-R-I) (Fragment)
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                                                                                                                                                                                              (POTENTIAL).
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1100
1121
1140
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351 AA;
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                                    28
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51
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143
163
206
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P79242;
                        Chemotaxis.
                                                TRANSMEM
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           FMLP TO THE RECEPTOR CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A G-PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM. SUBCELLULAR LOCATION: Integral membrane protein. SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 Q
WHICH ARE POWERFUL NEUTROPHILS CHEMOTACTIC FACTORS. BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 1782; DB 1; Length 348;
Pred. No. 1e-95;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                    InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Chemotaxis.
                                                                                                                                                                                                                                                                                                                                                                                      2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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5 (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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6 (POTENTIAL).
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CYTOPLASMIC (P
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47
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348 AA;
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TRANSMEM
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TRANSMEM
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SEQUENCE
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DOMAIN
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ö 61 YLNLALADFSFTATLPFLIVSWAMGEKWPFGWFLCKLIHIVVDINLFGSVFLIGFTALDR 120 TAVVASFFICWFPFQLVALLGTVWLKEMLFYGKYKIIDILVNPTSSLAFFNSCLNPMLYV 303 64 YLNLALADFSFTATLPFLIVSMAMGEKWPFGWFLCKLIHIVVDINLFGSVFLIGFIALDR 123 124 CICVLHPVWAQNHRTVSLAMKVIVGPWILALVLTLPVFLFLTTVTIPNGDTYCTFNFASW 183 Gaps 63 1 NFSTPLNEYEEGSYESAGYTVLRILPLVVLGVTFVLGVLGNGLVIWVAGFRMTRTVTTIC 60 NESTPLNEYEEVSYESAGYTVLRILPLVVLGVTFVLGVIGNGLVIWVAGFRWTRTVTTIC GGTPEERLKVAITMLTARGIIRFVIGFSLPMSIVAICYGLIAAKIHKKGMIKSSRPLRVL ; FVGQDFRERLIHSLPTSLERALSEDSAPTNDTAANSASPPAETELQAM 351 Matches 344; Conservative 241 184 181 244 304 셤 ò 셤 õ 셤 ò g ŏ g ò

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-i- FUNCTION: LOW AFFINITY RECEPTOR TO N-FORWYL-METHIONYL PEPTIDES, WHICH ARE POWERFUL NEUTROPHILS CHEMOTACTIC FACTORS. BINDING OF FMLP TO THE RECEPTOR CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A G-PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -1- SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                  Gorilla gorilla gorilla (Lowland gorilla).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
NCBI_TaxID=9595;
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CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . ) (POTENTIAL).
POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                 Alvarez V., Coto E., Sehen F., Gouzalek-Koces S., Lopez-Larrea "Molecular evolution of the N-formyl peptide and C5a receptors non-human primates.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Interpro; IPR000276; GPCR_Rhodpsn.
Pfam: PF00001; 7tm_1; 1.
PR051E; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PR05ITE; PS03052; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein;
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EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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                                                                                                  15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
FMLP-related receptor I (FMLP-R-I) (Fragment).
                                                     348 AA
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2; Mismatches
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CYTOPLASMIC (
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MEDLINE=96421539; Pubmed=8824156;
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98.9%;
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Matches 344;
                                                        FML1_GORGO
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CARBOHYD
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TRANSMEM
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RESULT 3
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                 243
                                                                                                                                         TAVVASFFICWFPFQLVALLGTVWLKEMLFYGKYKIIDILVNPTSSLAFFNSCLNPMLYV 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Immunogenetics 44:446-452(1996).

-1. FUNCTION: LOW AFFINITY RECEPTOR TO N-FORMYL-METHIONYL PEPTIDES, WHICH ARE POWERFUL NUGTROPHILS CHEMOTACTIC FACTORS. BINDING OF FALL OT THE RECEPTOR CAUGES ACTIVATION OF NEUTROPHILLS. THIS RESPONSE IS MEDIATED VIA A G-PROTEIN THAY ACTIVATES A PHOSPHATIDYLINOSITOL-CALCIUM SESCOND MASSENGER SYSTEM.
-1. SUBCELLULAR LOCATION: Integral membrane protein.
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                                                                                                                                                                                                  64 YLNLALADFSFTATLPFLIVSMAMGEKWPFGWFLCKLIHIVVDINLFGSVFLIGFIALDR
                                                            CICVLHPVWAQNHRTVSLAMKVIVGPWILALVLTLPVFLFLTTVTIPNGDTYCTFNFASW
                                                                                                                       GGTPEERLKVAITMLTARGIIRFVIGFSLPMSIVAICYGLIAAKIHKKGMIKSSRPLRVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alvarez V., Coto E., Sehen F., Gouzalek-Koces S., Lopez-Larrea C.; "Molecular evolution of the N-formyl peptide and C5a receptors in non-human primates.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pongo.
                                                                                                                                                                                                                                               FVGQDFRERLIHSLPTSLERALSEDSAPINDTAANSASPPAETELQAM 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 (POTENTIAL).
EXTRACELLUIAR (POTENTIAL).
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Interpro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein;
                                                                                                                                                                                                                                                               EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                   I (FMLP-R-I) (Fragment)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=96421539; PubMed=8824156;
                                                                                                                                                                                                                                                                                                                                                                                     (Rel. 36, Created)
(Rel. 36, Last sequ
(Rel. 36, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pongo pygmaeus (Orangutan).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X97744; CAA66328.1;
                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                  15-JUL 1998 (Rel. 36, C. 15-JUL-1998 (Rel. 36, L. 15-JUL-1998 (Rel. 36, L. FMLP-related receptor I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9600;
                                                                                                                                                                                                                                                                                                                                                       FML1_PONPY P79236;
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                                                                                                                                                                                                                                                                                                                                                183
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                                                                                                                                                                                                                             4 NFSTPLNEYEEVSYESAGYTVLRILPLVVLGVTFVLGVLGNGLVIWVAGFRMTRTVTTIC 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Immunogenetics 44:446-452(1996).

-I-FUNCTION: LOW AFFINITY RECEPTOR TO N-FORMYL-METHIONYL PEPTIDES, WHICH ARE POWERFUL NEUTROPHILS CHEMOTACTIC FACTORS. BINDING OF FMLP TO THE RECEPTOR CAUGES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A G-PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.

-I-SUBCELLULAR LOCATION: Integral membrane protein.

-I-SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                     184 GGTPEERLKVAITMLTARGIIRFVIGFSLPMSIVAICYGLIAAKIHKKGMIKSSRPLRVL
                                                                                                                                                                                                                                                                                                                                                                                                                      244 TAVVASFFICWFPFQLVALLGTVWLKEMLFYGKYKIIDILVNPTSSLAFFNSCLNPMLYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Macaca mulatta (Rhesus macaque).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                      64 YLNLALADFSFTATLPFLIVSMAMGEKWPFGWFLCKLIHIVVDINLFGSVFLIGFIALDR
                                                                                                                                                                                                                                                                                                                                             CICVLHPVWAQNHRTVSLAMKVIVGPWILALVLTLPVFLFLTTVTIPNGDTYCTFNFASW
                                                                                   CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                     .;
0
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                                                                                                                                                                       Length 348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FVGQDFRERLIHSLPTSLERALSEDSAPINDTAANSASPPAETELQAM 351
                                                                                                                                                                                                   Indels
  EXTRACELLULAR (POTENTIAL).
                                           6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                                                                                                                                           38686 MW; E5A4D005CFA41616 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                  7;
                                                                                                                                                                    Score 1744; DB 1;
Pred. No. 1.5e-93;
5; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
FMLP-related receptor I (FMLP-R-I) (Fragment)
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                                                                        7 (POTENTIAL).
CYTOPLASMIC (F
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                                                                                                                POTENTIAL.
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15-JUL-1998 (Rel. 36, Last seq
15-JUL-1998 (Rel. 36, Last ann
                                                                                                                                                                    96.0%;
illarity 96.6%;
Conservative
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202
223
223
263
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363
348
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348
348 AA;
                                                                                                                                                                                    Best Local Similarity
Matches 336; Conserv
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseelab-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                               CICVLHPVWAQNHRTVSLAMKVIVGPWILALVLTLPVFLFLTTVTIPNGDTYCTFNFASW 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  244 TAVVASFFICWFPFQLVALLGTVWLKEMLFYGKYKIIDILVNPTSSLAFFNSCLNPMLYV 303
                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                  GGTPEERLKVAITMLTARGIIRFVIGFSLPMSIVAICYGLIAAKIHKKGMIKSSRPLRVL
                                                                                                                                                                                                                                 7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
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15-JUL-1998 (Rel. 36, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
FMLP-related receptor I (FMLP-R-I) (Lipoxin A4 receptor) (LXAA
                                                                                                                                                                                                                                                                                            95.8%; Score 1740; DB 1; Length 348; 96.6%; Pred. No. 2.6e-93; ive 7; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   304 FVGQDFRERLIHSLPTSLERALSEDSAPINDTAANSASPPAETELQAM 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Interpro; IPR000276; GPCR_Rhodpsn.
Pfam: PF00001; 7tm_1: 1.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein;
                                                                                                                                                                        4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
                                                                                                                    EXTRACELLULAR (POTENTIAL).
                                                                                                                                              2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                           6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
7 (POTENTIAL)
                                                                                                                                                                                                                                                                            BC185DFAC14B694E CRC64;
                                                                                                                                                                                                         CYTOPLASMIC (POTENTIAL).
                                                                                                                                     CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                (POTENTIAL).
                                                                                                                                                                                                                                                                                                    Pred. No. 2.667; Mismatches
                                                                                                                                                               (POTENTIAL)
                                                                                                                              (POTENTIAL)
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                                                                                                                                                                                                                                                                            38456 MW;
                                         EMBL; X97737; CAA66321.1;
HSSP; P34996; 1DDD.
                                                                                                                                                                                                                                                                                                             Conservative
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348
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FPRL1 OR LXA4R.
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008790;
                                                                                                     Chemotaxis.
                                                                                                                                                                                                                                                                                                            Matches 336;
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FML1_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (LEUKOTRIENE B4).
--- SUBCELLULAR LOCATION: Integral membrane protein.
--- TISSUE SPECIFICITY: EXPRESSED MOSTLY IN NEUTROPHILS, FOLLOWED BY SPLEEN AND LUNG: EXPRESSED AT VERY LOW LEVELS IN HEART AND LIVER.
--- SIMILARITY: BELONGS TO FAMILY I OF G-PROTEIN COUPLED RECEPTORS.
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Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 METHFSTPLNEYEEVSYESAGYTVLRILPLVVLGVTFVLGVLGNGLVIWVAGFRMTRTVT
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N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
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                                                                                                                                                                                                                                                             Takano T., Fiore S., Maddox J.F., Brady H.R., Petasis N.A., Serhan C.N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65; Indels
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PROSTIE; PS00237; G_ROTEIN_RECEP_F1_1; 1.
PROSTIE; PS00253; G_ROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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Pred. No. 3e-70;
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InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
                                                                                                                                                   SEQUENCE FROM N.A.
TISSUE-Spleen, and Neutrophils;
MEDLINE-97296322; Pubmed-9151906;
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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73.2%;
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                                                                             NCBI_TaxID=10090;
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Matches 257;
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DISULFID
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                                                                                                  181 ASWGGTPEERLKVAITMLTARGIIRFVIGFSLPMSIVAICYGLIAAKIHKKGMIKSSRPL 240
                                                                                                               181 VSWGNSVEERLNTAITFVTTRGIIRFIVSFSLPMSFVAICYGLITTKIHKKAFVNSSRPF 240
                                                                                                                                                                     61 TIWYLNLALADFSFTATLPFLLVEMAMKEKWPFGWFLCKLVHIAVDVNLFGSVFLIAVIA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-94256976; PubMed=8198572;

Durstin M., Gao J.-L., Tiffany H.L., McDermott D., Murphy P.M.;

Differential expression of members of the N-formylepetide receptor gene cluster in human phagocytes.";

Biochem. Biophys. Res. Commun. 201:174-179(1994).

I-FUNCTION: LOW AFFINITY RECEPTOR TO N-FORMYL-METHIONYL PEPTIDES, WHICH ARE POWERFUL NEUTROPHILS CHEWOTACTIC FACTORS. BINDING OF FMLP TO THE RECEPTOR CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A G-PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.

I-SUBCELLUIAR LOCATION: Integral membrane protein.

SUBCELLUIAR LOCATION: Integral membrane protein.
                                                          LDRCICVLHPVWAQNHRTVSLAMKVIVGPWILALVLFLPVFLFLTTVTIPNGDTYCTFNF
                                                                                                                                                       RVLTAVVASFFICWFPFQLVALLGTVWLKEMLFYGKYKIIDILVNPTSSLAFFNSCLNPM
                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-92307681; PubMed-1612600; Bao L., Gerard C.; Bao L., Gerard N.P., Eddy R.L. Jr., Shows T.B., Gerard C.; "Mapping of genes for the human C5a receptor (C5AR), human FMLP receptor (FPRI), and two FMLP receptor homologue orphan receptors (FPRH1, FPRH2) to chromosome 19."; Genomics 13:437-440(1992).
301 LYVFVGQDFRERLIHSLPTSLERALSEDSAPTNDTAANSASPPAETELQAM 351
                                                                                                                                                                                                                            16-0CT-2001 (Rel. 40, Last sequence update)
FMLP-related receptor II (FMLP-R-II).
                                                                                                                                                                                                                                                                                                            353 AA.
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Pfam; PF00001; 7tm_1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
                                                                                                                                                                                                                                                                                                                                        Created)
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                                                                                                                                                                                                                                                                                                            STANDARD;
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Genew; HGNC:3828; FPRL2.
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                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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P25089;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-96421539; PubMed=8824156; Alvarez V., Coto E., Sehen F., Gouzalek-Koces S., Lopez-Larrea C.; Molecular evolution of the N-formyl peptide and C5a receptors in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 TICYLNLALADFSFTATLPFLIVSMAMGEKWPFGWFLCKLIHIVVDINLFGSVFLIGFIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LDRCICVLHPVWAQNHRTVSLAMKVIVGPWILALVLTLPVFLFLTTVTIPNGDTYCTFNF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pan troglodytes (Chimpanzee).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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                                                                                                                                                                                                                                                                  7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
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Pred. No. 3.7e-69;
9; Mismatches 59; Indels
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                                                                                                2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL)...
   G_PROTEIN_RECEP_F1_2; 1.
receptor; Transmembrane; Glycoprotein;
                                                   EXTRACELLULAR (POTENTIAL).
                                                                                                                                   3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL)..
                                                                                                                                                                  4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                     -> G (IN REF. 2).
-> S (IN REF. 2).
-> D (IN REF. 2).
8ED7450A14A36C9A CRC64;
                                                                   1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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15-JUL-1998 (Rel: 36, Last sequence update)
15-JUL-1998 (Rel: 36, Last annotation update)
N-formyl peptide receptor-like 2 receptor (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 3.7e
39; Mismatches
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71.78;
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266
286
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338 3
353 AA;
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Best Local Similarity
PROSITE; PS50262;
G-protein coupled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                     Chemotaxis.
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P79243;
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SEQUENCE
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Matches
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                                                                                                                                              PHOSPHATIDYLINGSITOL-CALCIUM SECOND MESSENGER SYSTEM.
SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                  Immunogenetics 44:446-452(1996).
-1- FUNCTION: LOW AFFINITY RECEPTOR TO N-FORMYL-METHIONYL PEPTIDES, WHICH ARE POWERFUL NEUTROPHILS CHEMOTACTIC FACTORS. BINDING OF FMLP TO THE RECEPPTOR CAUGES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A G-PROTEIN THAT ACTIVATES A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ASWGGTPEERLKVAITMLTARGIIRFVIGFSLPMSIVAICYGLIAAKIHKKGMIKSSRPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Pred. No. 8e-69;
37; Mismatches 58; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 G-protein coupled receptor; Transmembrane; Glycoprotein;
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EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (P
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CYTOPLASMIC (
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Pfam; PF00001; 7tm_1; 1.
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162
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226
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SEQUENCE
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SO THE PROPERTY OF THE PROPERT
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between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                -1- SUBCELLULAR LOCATION: Integral membrane protein.
-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                Immunogenetics 44:446-452(1996).

-i- FUNCTION: LOW AFFINITY RECEPTOR TO N-FORMYL-METHIONYL PEPTIDES, WHICH ARE POWERFUL NEDTROPHILS CHEMOTACTIC FACTORS. BINDING OF FMLP TO THE RECEPTOR CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A G-PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.
                                                                                                          Pongo pygmaeus (Orangutan).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
                                                                                                                                                                                                                     Alvarez V., Coto E., Sehen F., Gouzalek-Koces S., Lopez-Larrea C. "Molecular evolution of the N-formyl peptide and C5a receptors in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein;
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EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
                                                                            N-formyl peptide receptor-like 2 receptor (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71.8%; Score 1304; DB 1; 71.6%; Pred. No. 2.3e-68;
                             (Rel. 36, Created)
(Rel. 36, Last sequence update)
(Rel. 36, Last annotation update)
349 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                71.6%; Pred. No. 2.3e tive 39; Mismatches
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InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
                                                                                                                                                                                                       MEDLINE-96421539; PubMed-8824156;
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Matches 250; Conservative
 STANDARD;
                                                                                                                                                                                                                                                      non-human primates.";
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                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                         NCBI_TaxID=9600;
                               15-JUL-1998
                                                            15-JUL-1998
                                               15-JUL-1998
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 FML2_PONPY P79237;
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TRANSMEM
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                                                                                                                                                     180
                                                                                                                                     181 ASWGGTPEERLKVAITMLTARGIIRFVIGFSLPMSIVAICYGLIAAKIHKKGMIKSSRPL 240
                                                                                                                                                                                                                 241 RVFAAVVASFFICWFPYELIGILMAVWLKEMLLNGKYKIILVLLNPTSSLAFFNSCLNPI 300
              61 TICYLNLALADFSFTATLPFLIVSMAMGEKWPFGWFLCKLIHIVVDINLFGSVFLIGFIA 120
                                                                           LDRCICVLHPVWAQNHRTVSLAMKVIVGPWILALVLTLPVFLFLTTVTIPNGDTYCTFNF 180
                                                                                                                                                                                                  RVLTAVVASFFICWFPFQLVALLGTVWLKEMLFYGKYKIIDILVNPTSSLAFFNSCLNPM 300
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-1- FUNCTION: LOW AFFINITY RECEPTOR TO N-FORNYL-METHIONYL PEPTIDES,
WHICH ARE POWERFUL NEUTROPHILS CHEMOTACTIC FACTORS. BINDING OF
FMLP TO THE RECEPTOR CAUSES ACTIVATION OF NEUTROPHILS. THIS
RESPONSE IS MEDIATED VIA A G-PROTEIN THAT ACTIVATES A
PHOSPHATIDYLINGOSITOL-CALCIUM SECOND MESSENGER SYSTEM.

-1- SUBCELULAR LOCATION: Integral membrane protein.

-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alvarez V., Coto E., Sehen F., Gouzalek-Koces S., Lopez-Larrea C., "Molecular evolution of the N-formyl peptide and C5a receptors in
                                                                                           Gorilla gorilla gorilla (Lowland gorilla).
Sukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Gorilla.
NCBI_TaxID=9595;
                                                                                                                                                                                                                                                              LYVFVGQDFRERLIHSLPTSLERALSE--DSAPTNDTAANSASPPAETE 347
                                                                                                                                                                                                                                                                             EMBL; X97742; CAA66326.1; -.
InterPro; IPR00275; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50263; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Chemotaxis.
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EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                      15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
FMLP-related receptor II (FMLP-R-II) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 (POTENTIAL).
CYTOPLASMIC (PO'
4 (POTENTIAL).
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SEQUENCE FROM N.A.
MEDLINE=96421539; Pubmed=8824156;
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15-JUL-1998 (Rel. 36, Last sequ
15-JUL-1998 (Rel. 36, Last anno
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P79178;
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                      modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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P21462: Q14939; Q9NS48:
01-MAY-1991 (Rel. 18, Created)
01-MAY-1991 (Rel. 18, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
fMct-Leu-Phe receptor (fMLP receptor) (N-formyl peptide receptor)
FPR) (N-formylpeptide chemoattractant receptor).
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N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
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European Bioinformatics Institute. There are no rest
by non-profit institutions as long as its content
                                                                       EMBL; X97740; CAA66324.1; -.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
PROSITE; PS0037; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50263; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein;
                                                                                                                                                                                                                                                                        EXTRACELLULAR (POTENTIAL). 5 (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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70.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

Lamerdin J.E., McCready P.M., Skowronski E., Viswanathan V.,

Lamerdin J.E., McCready P.M., Dias J., Ramirez M., Stilwagen S.,

Phan H., Velasco N., Do L., Regala W., Terry A., Brower A., Garnes J.,

Danganan L., Erler A., Christensen M., Georgescu A., Avila J., Liu S.,

Andreise T., Trankheim M., Attix C., Amico Keller G., Coeffeld J.,

Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Kronmiller B.,

Arellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A.,

Sequence analysis of a 5-Mb region in 19q13.4.";

Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strausberg R.;
Submitted (MRY-2001) to the EMBL/GenBank/DDBJ databases.

- FUNCTION: HIGH AFFINITY RECEPTOR FOR N-FORMIL-METHIONIL PEPTIDES,
WHICH ARE POWERFUL NEUTROPHILS CHEMOTACTIC FACTORS. BINDING OF
FMLP TO THE RECEPTOR CAUSES ACTIVATION OF NEUTROPHILS. THIS
RESPONSE IS MEDIATED VIA A G-PROTEIN THAT ACTIVATES A
PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.
- SUBCELLULAR LOCATION: Integral membrane protein.
- TISSUE SPECIFICITY: NEUTROPHILS.
- POLYMORPHISM: THE VARIANT SOUDENCES ARE THOUGHT TO BE DUE TO
ALLELIC VARIATION OF A SINGLE GENE.
- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                 SEQUENCE FROM MILE-90267449; PubMed-2161213; MEDLINE-90267449; PubMed-2161213; Boulay F., Tardif M., Brouchon L., Vignais P.; Synthesis and use of a novel N-formyl peptide derivative to isolate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE-94040825; Pubmed-8224916;
Murphy P.M., Tiffany H.L., McDermott D., Ahuja S.K.;
"Sequence and organization of the human N-formyl peptide receptor-
                                      Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                   MEDLINE-91105045; PubMed-2176894;
Boulay F., Tardif M., Brouchon L., Vignais P.,;
"The human N-formylpeptide receptor. Characterization of two CD isolates and evidence for a new subfamily of G-protein-coupled
                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE-91286286; PubMed-1712023;
Murphy P.M., McDermott D.;
Functional expression of the human formyl peptide receptor in Xenopus oocytes requires a complementary human factor.";
J. Biol. Chem. 266:12560-12567(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (MAR-1993) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                        a human N-formyl peptide receptor cDNA.";
Biochem. Biophys. Res. Commun. 168:1103-1109(1990).
                                                                                                                                                                                                                                                                                                                                                                                           Biochemistry 29:11123-11133(1990)
sapiens (Human).
                                      Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    encoding gene.";
Gene 133:285-290(1993).
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                                                                               NCBI_TaxID=9606;
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TICYLNLALADFSFTATLPFLIVSMAMGEKWPFGWFLCKLIHIVVDINLFGSVFLIGFIA 120
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N-LINKED (GLCNAC. . ) (POTENTIAL)
N-LINKED (GLCNAC. . ) (POTENTIAL)
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PRINTS; PR00237; GPCRHODDPSN.
PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50267; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein;
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CYTOPLASMIC (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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0663EFF8267E2BD1 CRC64;
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CYTOPLASMIC (POTENTIAL).
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; Pred. No. 6.6e-65;
37; Mismatches 77
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CYTOPLASMIC (P
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EMBL, M37128; AAA36362.1; -.
EMBL, M60626; AAA35846.1; -.
EMBL, M60627; AAA3847.1; -.
EMBL, L10820; AAA16863.1; -.
EMBL, AC018755; AAF87842.1; -.
PIR, A35495; A35495.
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Matches 240; Conservative
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SPWTNDPKERINVAVAMLTVRGIIRFIIGFSAPMSIVAVSYGLIATKIHKQGLIKSSRPL 240 LDRCICVLHPVWAQNHRTVSLAMKVIVGPWILALVLTLPVFLFLTTVTIPNGDTYCTFNF 180 181 ASWGGTPEERLKVAITMLTARGIIRFVIGFSLPMSIVAICYGLIAAKIHKKGMIKSSRPL 240 RVLTAVVASFFICWFPFQLVALLGTVWLKEMLFYGKYKIIDILVNPTSSLAFFNSCLNPM 300 121 181 241 ద ò 셤 ò 셤 ò

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301 LYVFVGQDFRERLIHSLPTSLERALSEDSAPTNDTAANSASPPAETELQA 350 300 g δ g

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N-LINKED (GLCNAC. . .) (POTENTIAL) ä 67.4%; Score 1225.5; DB 1; Length 346; 68.6%; Pred. No. 7e-64; (FPR) (N-formylpeptide chemoattractant receptor) (Fragment) ; Pred. No. 7e-64; 35; Mismatches 73; Indels Pfam; PF00001; 7tm_1; 1.
PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE: PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Chemotaxis. EXTRACELLULAR (POTENTIAL). EXTRACELLULAR (POTENTIAL). 4 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

5 (POTENTIAL). EXTRACELLULAR (POTENTIAL). 97D3D7F45439BBD2 CRC64; 5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL). 1 (POTENTIAL). CYTOPLASMIC (POTENTIAL). (POTENTIAL). 346 AA (POTENTIAL). (POTENTIAL) 2 (POTENTIAL) CYTOPLASMIC POTENTIAL PRT; InterPro; IPR000276; GPCR_Rhodpsn. SEQUENCE FROM N.A. MEDLINE-96421539; Pubmed-8824156; MM. EMBL; X97745; CAA66329.1; -37986 Similarity 68.698; Conservative STANDARD; 346 346 346 346 346 AA; NCBI_TaxID=9598; 238; FMLR_PANTR DOMAIN TRANSMEM DISULFID NON_TER SEQUENCE DOMAIN TRANSMEM DOMAIN TRANSMEM **TRANSMEM** TRANSMEM TRANSMEM CARBOHYD Query Match TRANSMEM CARBOHYD NON_TER Local DOMAIN DOMAIN DOMAIN DOMAIN DOMAIN RESULT 13 FMLR_PANTR Matches Dp ŏ

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MONTHURATES.";
Immunogenetics 44:446-452(1996).

-!- FUNCTION: HIGH AFFINITY RECEPTOR FOR N-FORMYL-METHIONYL PEPTIDES,
WHICH ARE POWERFUL NEUTROPHILS CHEMOTACTIC FACTORS. BINDING OF
WHICH ARE POWERFUL NEUTROPHILS CHEMOTACTIC FACTORS.
FMLP TO THE RECEPTOR CAUSES ACTIVATION OF NEUTROPHILS. THIS
RESPONSE IS MEDIATED VIA A G-PROTEIN THAT ACTIVATES A
PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.
-!- SIBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics. Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                              243
                                                                                                                                  303
                                                                                                                                                                                        241 SFVAAAFFLCWSPYQVVALIATVRIRELL-OCMYKEIGIAVDVTSALAFFNSCLNPMLYV 299
           YLNLALADFSFTATLPFLIVSMAMGEKWPFGWFLCKLIHIVVDINLFGSVFLIGFIALDR 123
                                                                124 CICVLHPVWAQNHRTVSLAMKVIVGPWILALVLTLPVFLFLTTVTIPNGDTYCTFNFASW 183
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                                                                                                                                                                          TAVVASFFICWFPFQLVALLGTVWLKEMLFYGKYKIIDILVNPTSSLAFFNSCLNPMLYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-96421539; Pubmed-8824156;
Alvarez V., Coto E., Sehen F., Gouzalek-Koces S., Lopez-Larrea C.,
"Molecular evolution of the N-formyl peptide and C5a receptors in
                                                                                                                                                                                                                                                                                                                                                 15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-COT-2001 (Rel. 40, Last annotation update)
16-COT-2001 (Rel. 40, Last encorpton)
17-COT-2001 (RMLP recepton)
18-COT-2001 (N-formyl peptide recepton)
18-COT-2001 (Fragment)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
                                                                                                                                                                                                                           304 FVGQDFRERLIHSLPTSLERALSEDSAPTNDTAANSASPPAETELQA 350
                                                                                                                                                                                                                                          PROSITE; PS00237; G_FROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein;
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2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
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InterPro; IPR000276; GPCR_Rhodpsn.
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P79235;
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FMLR_PONPY
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REGULANCE FROM N.A.

REGULANCE FROM N.A.

REGULANCE—93163563; PubMed-8432964;

RA YE R.D., Quehenberger O., Thomas K.M., Navarro J., Cavanagh S.L.,

RA Prossnitz E.R., Cochrane C.G.;

RA Prossnitz E.R., Cochrane C.G.;

RT = The rabbit neutrophil N 'formy' peptide receptor. cDNA cloning,

RT = The rabbit neutrophil N 'formy' peptide receptor. cDNA cloning,

RT = The rabbit neutrophil N 'formy' peptide receptor. CDNA cloning,

RT = The rabbit neutrophil N 'formy' peptide receptor. CDNA cloning,

RT = The rabbit neutrophil N 'formy' peptide receptor. CDNA cloning,

RT = The rabbit neutrophil N 'formy' peptide receptor. CDNA cloning,

RT = The rabbit neutrophil N 'formy' peptide receptor. CDNA CLONING OF PULL RECEPTOR CAUSES ACTIVATION OF NEUTROPHILS. THIS

RESPONSE IS MEDIATED VIA A G-PROTEIN THAT ACTIVATES A

PHOSCHAATIOVIALNOSITOL. CALCIUM SECOND MESSERNER SYSTEM.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        124 CICVLHPVWAQNHRTVSLAMKVIVGPWILALVLTLPVFLFLTTVTIPNGDTYCTFNFASW 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        184 GGTPEERLKVAITMLTARGIIRFVIGFSLPMSIVAICYGLIAAKIHKKGMIKSSRPLRVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         244 TAVVASFFICWFPFQLVALLGTVWLKEMLFYGKYKIIDILVNPTSSLAFFNSCLNPMLYV
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Last annotation update)
Last annotation update)
Last receptor (MMP receptor) (N-formyl peptide receptor)
(FPR) (N-formylpeptide chemoattractant receptor).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oryctolagus cuniculus (Rabbit).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
                                                                                                                                                                                                        CYTOPIASMIC (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 346;
                                                                                                                                                                                                                                                                                                                                                                                                 67.4%; Score 1225.5; DB 1; Length
68.9%; Pred. No. 7e-64;
iive 34; Mismatches 73; Indels
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EXTRACELLULAR (POTENTIAL).
                                                                                                                                 6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                               38038 MW; A012EB86BAA7B315 CRC64;
  CYTOPLASMIC (POTENTIAL).
                                                                             5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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01-FEB-1994 (Rel. 28, Last sequancoursection)
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                                                                                                                                                                                                                                                                                                                                                  346 AA;
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Q05394;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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-i- TISSUE SPECIFICITY: NEUTROPHILS.
-i- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . ) (POTENTIAL)
N-LINKED (GLCNAC. . ) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67.3%; Score 1223.5; DB 1; Length 352; 67.7%; Pred. No. 9.3e-64; Live 41; Mismatches 70; Indels 3;
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                                                                                                                                                                                                              PRINTS; PRO0237; GPCRHODOPSN.
PROSTIE; PS00237; G_PCRHODOPSN.
PROSTIE; PS00237; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein;
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EXTRACELLULAR (POTENTIAL).
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5 (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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51DA550DAB13A091 CRC64;
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
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Matches 239; Conservative
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completed: December 16, 2002, 17:18:28 ne: 16 secs Search cor Job time

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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December 16, 2002, 17:17:02; Search time 34 Seconds (without alignments) 2127.133 Million cell updates/sec OM protein - protein search, using sw model Run on:

US-09-944-807-2 1817 Title: Perfect score: Sequence:

1 METHFSTPLNEYEEVSYESA......TNDTAANSASPPAETELQAM 351

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

671580 seqs, 206047115 residues Searched:

otal number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SPTREMBL_21:* Database :

sp_rodent:*
sp_rodent:*
sp_virus:*
sp_unclassified:*
sp_rvirus:*
sp_bacteriap:*
sp_archeap:* 1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:* 10: 112: 123: 144: 115: 176:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	O88536 mus culu	O88535 mus musculu		O88538 mus musculu	O9qwq9 cavia porce	0951h1 macaca fasc	O9pvy7 anguilla an	093247 cyprinus ca	Q9qln9 pan troqlod	Q8tbk4 homo sapien	Q9epp3 cavia porce	Q9mzm5 pithecia pi	Q9mzp1 mandrillus	Q9tsq8 cercopithec	Q9mzp3 presbytis e	Q9mzml eulemur mac
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ΩI	088536	088535	088537	08823	69WG60	Q95LH1	. 09PV	09324	O9GLN9	Q8TBK4	09EPE	Q9MZM5	Q9MZP1	30SI60	O9MZP3	о9м2м
BO	11	11	11	11	11	9	13	13	9	4	11	9	9	9	9	9
% Query Match Length DB	. 351	347	343	323	475	355	359	353	359	359	359	347	347	352	347	347
% Query Match	78.2	72.9	62.8	61.0	30.2	27.5	25.2	23.8	23.5	23.5	23.3	23.3	23.2	23.5	23.2	23.2
Score	1420	1325	1140.5	1107.5	549.5	200	457.5	433	427.5	426.5	423.5	422.5	421.5	421.5	421	421
Result	1	7	m	4	Ŋ	9	7	6 0	σ	10	11	12	13	14	15	16

09n1p4 cercopithec 09mzq3 pygathrix a 09mzq2 rhiopithec 09mzq1 pygathrix b 09mzq1 pygathrix n 09mzp9 nasalis lar 09mzp9 nasalis lar 09mzp5 presbytis p 09mzp4 presbytis p 09mzp4 madrillus 09mzp9 macaca assa 09mzp8 macaca assa 09mzp8 macaca arct 09mzp8 macaca arct 09mzp8 macaca chib 09mzn9 macaca chib 09mzn9 macaca neme	ന ഥന
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ALIGNMENTS

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61 TICYLNLALADFSFTATLPFLIVSMAMGEKWPFGWFLCKLIHIVVDINLFGSVFLIGFIA 120

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RVLTGVVASFFICWFPFQLVALLGTVWLKEMQFSGSYKIIGRLVNPTSSLAFFNSCLNPM 296
                          301 LYVFVGQDFRERLIHSLPTSLERALSEDSAPTNDTAANSASPPAETELQAM 351
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                                                                                                             PRELIMINARY;
                                                                                                                                                                                              Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                  Receptor.
SEQUENCE
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                                                                                                           088537
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            TIWYLNLALADFSFTATLPFILVEMAMKEKWPFGWFLCKLVHIVVDVNLFGSVFLIALIA 120
                                              181 ASWGGTPEERLKVAITMLTARGIIRFVIGFSLPMSIVAICYGLIAAKIHKKGMIKSSRPL 240
                                                                                               RVLTAVVASFFICWFPFQLVALLGTVWLKEMLFYGKYKIIDILVNPTSSLAFFNSCLNPM 300
                                                                                                                                                61 TICYLNLALADFSFTATLPFLIVSMAMGEKWPFGWFLCKLIHIVVDINLFGSVFLIGFIA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LDRCICVLHPVWAQNHRTVSLAMKVIVGPWILALVLTLPVFLFLTTVTIPNGDTYCTFNF 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LDRCICVLHPVWAQNHRTVSLAMKVIVGPWILALVLTLPVFLFLTTVTIPNGDTYCTFNF 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LDRCICVLHPVWAQNHRTVSL----VVGSWIFALILTLPLFLFLTTVRDARGDVHCRLSF 176
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                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-98390190; PubMed-9722950;
MEDLINE-98390190; PubMed-9722950;
Gao J.L., Chen H., Filie J.D., Kozak C.A., Murphy P.M.;
Gao J.L., Chen H., Filie J.D., Kozak C.A., Murphy P.M.;
Gao Millerential expansion of the N-formylpeptide receptor gene cluster in human and mouse.";
Genomics 5.1270-276(1998).
Genomics 5.1270-276(1998).
MGD; MGI:1278320; Fpr-rs1.
InterPro; RF0010276; GPCR_Rhodpsn.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 METNFSTPLNEYEEVSYESAGYTVLRILPLVVLGVTFVLGVLGNGLVIWVAGFRMTRTVT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ASWGGTPEERLKVAITMLTARGIIRFVIGFSLPMSIVAICYGLIAAKIHKKGMIKSSRPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4;
Length 347;
                                                                                                                                                                                301 LYVFVGQDFRERLIHSLPTSLERALSEDSAPTNDTAANSASPPAETELQA 350
                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             347 AA; 39071 MW; A755BF9F09575A70 CRC64;
                                                                                                                                                                                                                                                                                        01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1999 (TrEMBLrel. 08, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
N-formylpeptide receptor-like 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    72.9%; Score 1325; DB 11
73.2%; Pred. No. 2.8e-107
ive 27; Mismatches 63
                                                                                                                                                                                                                                                                    347 AA
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PRINTS; PR01559; DUFFYANTIGEN.
PRINTS; PR00237; GPCRRHODOPSN.
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Matches 257; Conservative
                                                                                                                                                                                                                                                                   PRELIMINARY;
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SEQUENCE
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TICYLNLALADFSFTATLPFLIVSMAMGEKWPFGWFLCKLIHIVVDINLFGSVFLIGFIA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RVLTAVVASFFICWFPFQLVALLGTVWLKEMLFYGKYKIIDILVNPTSSLAFFNSCLNPM 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE=98390190; PubMed=9722950; Gao J.-L., Chen H., Filie J.D., Kozak C.A., Murphy P.M.; "Differential expansion of the N-formylpeptide receptor gene cluster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 METNESTPLNEYEEVSYESAGYTVLRILPLVVLGVTFVLGVLGNGLVIWVAGFRMTRTVT 60
                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 ESVVANPĒGLKVSTTVSTATGIISFINCPSLPMSFIAVCYGLMAAKICRKGFLNSSRPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LYVFVGQDFRERLIHSLPTSLERALSEDSAPTNDTAANSASPPAETEL 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             343 AA; 38111 MW; 0F726BF195CBFB29 CRC64;
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Last sequence update)
Last annotation update)
                                                                                                                                                                                         01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
N-formylpeptide receptor-like 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MGD; MGI:1278318; Fpr-rs3.
InterPro: IRR000276; GPCR_Rhodpsn.
PRAM: PP00001; 7tm.1, 1.
PRINTS: PR00237; GPCRRHODOPSN.
PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
PROSITE: PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                343 AA
                                                                                                                                                PRT;
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Genomics 51:270-276(1998).
EMBL; AF071181; AAC34586.1; -.
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01-NOV-1998 (TrEMBLrel. 08,
01-NOV-1998 (TrEMBLrel. 08,
01-JUN-2002 (TrEMBLrel. 21,
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Matches 227; Conservative
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355 AA;
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                                                                          Receptor.
SEQUENCE
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SEQUENCE
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STRAIN=HARTLEY; TISSUE=SPLEEN;
MEDLINE=98041293; PubMed=9743361;
Fukuoka Y., Ember J.A., Hugli T.E.;
Fukuoka I., Ember J. Seforms of the guinea pig C3a anaphylatoxin
"Molecular cloning of two lasforms of the guinea pig C3a anaphylatoxin
receptor: alternative splicing in the large extracellular loop.";
J. Immunol. 161:2977-2984(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                181 ASWGGTPEERLKVAITMLTARGIIRFVIGFSLPMSIVAICYGLIAAKIHKKGMIKSSRPL 240
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                                                                                                                                                                                                                                                                                                                                                             MEDLINE-98390190; PubMed-9722950;
Gao J.-L., Chen H., Fille J.D., Kozak C.A., Murphy P.M.;
"Differential expansion of the N-formylpeptide receptor gene cluster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                  1 METNESTPLNEYEEVSYESAGYTVLRILPLVVLGVTFVLGVLGNGLVIWVAGFRMTRTVT
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
                                                                                                                                                                                                                                                                                              61.0%; Score 1107.5; DB 11; Length 323; 65.5%; Pred. No. 2.1e-88; 1ve 39; Mismatches 69; Indels 5;
                                                                                                                                                                                                                                                                        CC90EC09B4725036 CRC64;
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                                                                                                                                            Genomics 51:270-276(1998).

BEMBL; AR071182; AAC34587.1; -

MGD; MGI:12780317; FPI-rs4.

InterPrc; IRR000276; GPCR_Rhodpsn.

PRINTS; PR01559; DUFFYANTIGEN.

PRINTS; PR01559; DUFFYANTIGEN.

PROSITE; PS00237; GPCRRHODOPSN.

PROSITE; PS50262; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
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LYVFLGGEFRDRLIYSLYASLERALRED 323
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N-formylpeptide receptor-like 4.
                                                                                                                                                                                                                                                             Receptor.
SEQUENCE 323 AA; 36299 MW;
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Matches 215; Conservative
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                                                                                                                                     in human and mouse.
                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10141;
                                                            NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           232 GMIKS-SRPLRVLTAVVASFFICWFPFQLVALLGTVWLKEMLFYGKYKIIDILVNPTS-- 288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DRCICVLHPVWAQNHRTVSLAMKVIVGPWILALVLTLPVFLFLTTVTIPNGDTYCTFNFA 181
                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                     ETNFSTPLNEYEEVSYESAGYTVLRILPLVVLGVTFVLGVLGNGLVIWVAGFRMTRTVTT 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   298 LSTPEPPQDFWDDLSPFTHEYRTPRLLKVITFTRLVVGFLLPMIIMVACYTLIIFRMRRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              macaca rascicularis (Crab eating macaque) (Cynomolgus monkey).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria, Primates; Catarrhini; Cercopithecidae;
Mecaca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --EERLKVAITMLTARG------
                                                                                                                                                                                                                                                                                        Query Match 30.2%; Score 549.5; DB 11; Length 475; Best Local Similarity 28.8%; Pred. No. 1e-39; Matches 136; Conservative 61; Mismatches 104; Indels 171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          function as SIV/SHIV co-receptors, from cynomolgus macaque
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ------SLAFFNSCLNPMLYVFVGQDFRERLIHSLPTSLERALSED 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AF1292382; AAK97052.1; -. InterPro; IRR00276; GPCR_Rhodpsn. Pf00001; 7tm_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41370 MW; 1DDE41BE9CAC525C CRC64;
                                                                                                                                                                                                                             475 AA; 53528 MW; 2C2C4D6C02170726 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
EMBL; U86378; AAC36503.1; -.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7Tm_11; 1.
PRINTS; PR00237; GPCRTEIN_RECEP_F1_1; UNKNOWN_1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
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Query Match
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                                                           49 WVAGFRWTRTVTTICYLNLALADFSFTATLPFLIVSMAMGEKWPFGWFLCKLIHIVVDIN 108
                                                                    109 LFGSVFLIGFIALDRCICVLHPVWAQNHRTVSLAMKVIVGPWILALVLTLPVFLFLTTVT 168
                                                                                                 169 IPNGDTYCTFNFASWGGTPEERLKVAITMLTARGI--IRFVIGFSLPMSIVAICYGLIAA 226
                                                                                                                                KIHKKGMIKSSRPLRVLTAVVASFFICWFPFQLVALLGTVWLKEMLFYGKYK--IIDILV 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83 VSMAMGEKWPFGWFLCKLIHIVVDINLFGSVFLIGFIALDRCICVLHPVWAQNHRTVSLA 142
                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                              1 METNFSTPLNEYEEVSY------ESAGYTVLRILPLVVLGVTFVLGVLGNGLVI 48
                                      Anguilla anguilla (European freshwater eel).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Anguilliformes; Anguillidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24 VLRILPLVVLGVTFVLGVLGNGLVIWVA-GFRMTRTVTTICYLNLALADFSFTATLPFLI 82
                                                                                                                                                                                                                                                                                                                                                                                                                      39;
               30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 13; Length 359;
Length 355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59; Mismatches 126; Indels
               Indels
                                                                                                                                                                                  NPTSSLAFFNSCLNPMLYVFVGQDFRERLIHSLPTSLERALSEDS 329
                                                                                                                                                                                          Last sequence update)
Last annotation update)
               69; Mismatches 132;
Score 500; DB 6;
Pred. No. 1.5e-35;
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34.7%; Pred. No. 7.6e-32;
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Score 500;
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01-WAY-2000 (TrEMBLrel. 13, Last sequ
01-WAR-2002 (TrEMBLrel. 20, Last anno
27.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
               Matches 114; Conservative
                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                           Angiotensin receptor.
       Similarity
                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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Matches 119; Conserv
                                                                                                                                                                                                                                                                                                                NCBI_TaxID=7936;
Query Match
Best Local S
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13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HPVWAQNHRTVSLAMKVI-VGPWILALVLTLPVFLFLTTVTIPNGDTYCTFNFASWGGTP 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vertebrata; Euteleostomi;
Ostariophysi; Cypriniformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 NEYEEVSYESAGYTVLRILPLVVLGVTFVLGVLGNGLVIWVAGF-RMTRTVTTICYLNLA 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INTURNOGENETICS 49:909-914 (1999).
-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
EMBL, AB012310; BAA327971.
-1 InterPro; IPR000276; GPCR_Rhodpsn.
MKVIVGPWILALVLTLPVFLFLTTVTI--PNGDTYCTFNFASWGGTPEERLKVAITMLTA
                                                                                                 201 RGIIRFVIGFSLPMSIVAICYGLIAAKIHKKGMIKSSRP----LRVLTAVVASFFICWF
                                                                                                                                                                                            PFQLVALLGTV-WLKEMLFYGKYKIIDILVNPTSSLAFFNSCLNPMLYVFVGQDFRERLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDILNE=99367403; PubMed=10436187;
Fujiki K., Shin D., Nakao M., Yano T.;
"Molecular cloning of carp (Cyprinus carplo) CC chemokine, CXC
Chemokine receptors, allograft inflammatory factor-1, and natural
killer cell enhancing factor by use of suppression subtractive
hybridization.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 353;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Pred. No. 1e-29;
66; Mismatches 114; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PRO1556; CHEWOKINER1.
PRINTS; PRO1556; CHEWOKINER1.
PRINTS; PRO1556; CPCRHODOPSN.
PROSTTE; PRO1567; CPCRHODOPSN.
PROSTTE; PS500237; C_PROTEIN_RECEP_F1_1; 1.
PROSTTE; PS50262; C_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Glycoprotein; Transmembrane.
SEQUENCE 353 AA; 39633 MW; 849248E413FB3B3F CRC64;
                                                                                                                                                                                                                                                                                                                                                        -----HSLP----TSLERALSEDSAPTNDTAANS 339
                                                                                                                                                                                                                                                                                                                                                                                                    313 RLLRCGPGSAARHSHPSLTTKMSTLSYRASETLRLTSGKAASS 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08, Last sequence update)
21, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cyprinus carpio (Common carp).
Eukaryota; Metazoa; Chordata; Craniata;
Actinopterygii; Teleostei;
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Matches 112; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               154 LVLTLPVFLFLTTVTIPNGD-TYCTFNFASWGGTPEERLKVAITMLTARGIIRFVIGFSL 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----VWKAVFRFQHIFVGFLLPGLIILTCYCIIISKLSKNSKGQALKRKALKT 243
                                                                                                                                 LTAVVASFFICWFPFQLVALLGTV------WLKEMLFYGKYKIIDILVNPTS 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : ||:|: || ||: || || :| || :| ||: || ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the renin angiotensin system.";
Genomics 69:14-26(2000).
-- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY)
-- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
EMBL, AF193445; AAG28410.1;
-- HSSP; P34996; 1DDD.
InterPro; IPR000276; GPCR_Rhodpsn.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LKEMLFYGKYK-----IIDILVNPTSSLAFFNSCLNPMLYVFYGODFRE---RLIHSLP
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                                                                                                                                                                                                                                                                       Pan troglodytes (Chimpanzee).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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                                                                                                                                                                                                                                   SLAFFNSCLNPMLYVFVGQDFRERLIHSL - - - PTSLERALSEDSAPTNDTAANSAS
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PRINYS; PR00237; GPCRRHODOPSN.
PROSTITE; PS050223; G_PROTEIN_ERCEP_F1_1; 1.
G-protein coupled receptor; Glycoprotein; Receptor; Triscoprotein coupled and the secoptor; Glycoprotein; Receptor; Triscoprotein; Receptor; Triscoprotein coupled and the secoptor; Glycoprotein; Receptor; Triscoprotein coupled and the secoptor; Glycoprotein; Receptor; Triscoprotein and the secoptor; Glycoprotein; Receptor; Triscoprotein and the secoptor; Glycoprotein and the secoptor and the second and the seco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-20469400; PubWed-11013071;
Dufour C., Casane D., Denton D., Wickings J., Corvol
Jeunemaitre X.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 23.5%; Score 427.5; DB 6; Best Local Similarity 31.0%; Pred. No. 3.1e-29; Matches 103; Conservative 69; Mismatches 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   359 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----TSLERALSEDSAPTNDTAANSASPPA 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PKAKSHSNLSTKMSTLSYRPSDNVSSSTKKPA 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Angiotensin II type-1 receptor AGTR1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TrEMBLrel. 16, TrEMBLrel. 16, (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID-9598;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -MAR-2001
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01-MAR-2002
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                                                                             243
    195
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Q9GLN9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            154 LVLTLPVFLFLTTVTIPNGD-TYCTFNFASWGGTPEERLKVAITMLTARGIIRFVIGFSL 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             268 IKEMLFYGKYK-----IIDILVNPTSSLAFFNSCLNPMLYVFVGQDFRE---RLIHSLP 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             265 ---LIQLGIIRDCRIADIVDTAMPITICIAYFNNCLNPLFYGFLGKKFKRYFLQLLKYIP 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35 VTFVLGVLGVLGVLWVAGFRM-TRTVTTICYLNLALADFSFTATLPFLIVSMAMGEKWPF 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Busmann A., Noack T., Zucht HD., Forssmann W.G., Meyer M.; "Isolation of Angiotensin I from human hemofiltrate as a potent modulator of KATP channels."; Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
EMBL; AJ301623; CAC21550.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        213 PMSIVAICYGLIAAKIHKKGMIKSSRP----LRVLTAVVASFFICWFPFQLVALLGTVW
                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostc
Mammalia; Eutheria; Rodentia; Hystricognathi; Cavildae; Cavia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68; Mismatches 124; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strausberg R.; Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases EMBL; BC022447; AAH22447.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        359 AA; 41087 MW; AF90BE7F21E911BA CRC64;
                                                                        21, Created)
21, Last sequence update)
21, Last annotation update)
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(TrEMBLrel. 16, Last sequence update)
(TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 426.5; DB 4
Pred. No. 3.8e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ş
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     322 PKAKSHSNLSTKMSTLSYRHSDNVSSSTKKPA 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23.5%;
31.0%;
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    PRELIMINARY;
                                                                                                            (Tremblrel.
                                                                                                                                                    (TrEMBLrel.
                                                                            (TrEMBLrel.
                                                                    01-JUN-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
Angiotensin receptor 1.
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                                                                                                                                                                                                                                Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
TISSUE=BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10141;
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                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2001
01-MAR-2001
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Receptor.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                            Q8TBK4;
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Q8TBK4
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6

11;

Gaps

Indels

Length 347;

84

193 197 306

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SEQUENCE FROM N.A.
Zheng X.-Z., Zhang Y.-P., Geng Z.-C.;
"Molecular Evolution of the Chemokine Receptor CXCR4 Gene Sequences in
                                                                                                                                                                                                                                                                                       85 MAMGEKWPFGWFLCKLIHIVVDINLFGSVFLIGFIALDRCICVLHPVWAQNHRTVSLAMK 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 | | : : : | | :: | | :: | 246 CWLPYYIGISIDSFILLEIIRQGCEFENTVHKWISI----TEALAFFHCCLNPILYAFLG 301
                                                                                                                                                                                                RILPLVVLGVTFVLGVLGVLGNGLVIWVAGF-RMTRTVTTICYLNLALADFSFTATLPFLIVS 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY)
--- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
EMBL; AF172222; AAF89342.1; --
InterPro; IPR000276; GPCR_Rhodpsn.
InterPro; IPR003006; Ig_MHC.
                                                                                                                                                             26 RILPLVVLGVTFVLGVLGNGLVIWVAGF-RMTRTVTTICYLNLALADFSFTATLPFLIVS
                                                                                                                                                                                                                                                                                                                       145 VI-VGPWILALVLTLPVFLFLTTVT-----IPNGDTYCTFNFASWGGTPEERLKV
                                                                                                                                                                                                                                                                                                                                                                                                                                              194 AITMLTARGIIRFVIGFSLPMSIVAICYGLIAAKI-HKKGMIKSSRPLRVLTAVVASFFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00001; 7th_1; 7.

PRINTS; PR01558; CHEMOKINER1.

PRINTS; PR01558; CHEMOKINER1.

PRO1575; PR01568; LIMPHOTACTUR.

PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.

PROSITE; PS00290; IG_MHC; UNKNOWN_1.

G-PFO161in coupled receptor; Glycoprotein; Receptor; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               253 CWFPFQLVALLGTVWLKEMLFYG-----KYKIIDILVNPTSSLAFFNSCLNPMLYVFVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
Cercopithecinae, Mandrillus.
NCBI_TaxID=9568;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23.2%; Score 421.5; DB 6; Length 33.1%; Pred. No. 9.9e-29; ive 56; Mismatches 107; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        347 AA; 39273 MW; OAE9714D1B5655B4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mandrillus leucophaeus (Drill) (Papio leucophaeus).
                                             DB 6;
                                      23.3%; Score 422.5; DB 6
33.1%; Pred. No. 8.1e-29;
ive 55; Mismatches 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              347 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      307 ODFRERLIHSLPTSLERALS 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             302 AKFKTSAQHAL-TSVSRGSS 320
                                                                                                      Conservative
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                                                                      Local Similarity
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                                                                   Best Local Sim
Matches 106;
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Best Local (
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Q9MZP1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GWFLCKLIHIVVDINLFGSVFLIGFIALDRCICVLHPVWAQNHRTVSLAMKVIVGPWILA 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      154 LVLTLPVFLFLTTVTIPNGD-TYCTFNFASWGGTPEERLKVAITMLTARGIIRFVIGFSL 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | |: | | | | : | |: ::|
PFLIILTSYTLIWKALKKAYEIQKNKPRNDDIFKIIMAIVLFFFFSWVPHQIFTFLDVLI 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       267 QLGIIHDCKISDIVDTAMPITICIAYFNNCLNPLFYGFLGKKFKKYFLQLLKYIPPKAKS 326
                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                           35 VTFVLGVLGNGLVIWVAGFRM-TRTVTTICYLNLALADFSFTATLPFLIVSMAMGEKWPF 93
                InterPro; iPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
PRNINTS; PR00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS00202; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
SEQUENCE 359 AA; 41045 MW; D00F4C2C472DE5CC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ::|| : | | : | | : : | | : : || 157 GLASLPAVIHRNVFFIENTNITVCAFHYESQNST----LPIGL-----GITKNILGFWF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PMSIVAICYGLIAAKIHKKGMIKSSRP----LRVLTAVVASFFICWFPFQLVALLGTVW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LKEMLFYGKYK-IIDILVNPTSSLAFFNSCLNPMLYVFVGQDFRE---RLIHSLP----
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Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Pitheciinae;
                                                                                                                                                                                                                                                                                                                                                 27;
                                                                                                                                                                                                                                                                                 DB 11; Length 359;
                                                                                                                                                                                                                                                                              23.3%; Score 423.5; DB 11; Length 30.8%; Pred. No. 6.9e-29; ive 72; Mismatches 128; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                347 AA; 39290 MW; E59B2070BF0F58E4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              319 -TSLERALSEDSAPTNDTAANSASPPAE 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        327 HSTLSTKMSTLSYRPSNNVSSSAKKPVQ 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pithecia pithecia (White-faced saki).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-0CT_2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last seq
01-JUN-2002 (TrEMBLrel. 21, Last ann
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                                                                                                                                                                                                                                                                                                              Best Local Similarity 30.89
Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                          Similarity
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                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                           RA SEQUENCE FROM N.A.

RA PSEQUENCE FROM N.A.

RA HOLKAMD N., Baier M., Werner A.;

RU CXCR4 from African green monkey.";

RL SUBMITTEG (AUG-1997) to the EMBL/GenBank/DDBJ databases.

CC -1- SIMILARITY: BELONGS TO FRAILY 1 OF G-PROTEIN (BY SIMILARITY).

CC -1- SIMILARITY: BELONGS TO FRAILY 1 OF G-PROTEIN COUPLED RECEPTORS.

DR EMBL; AF019378; AAD01638.1; -1.

DR INTER-PO: IPR000276; GPCR_Rhodpsn.

DR PRINTS; PR01556; CHEMORINER11.

PRINTS; PR01568; CHEMORINER11.

PRINTS; PR01568; LYMPHOTACTUR.

R PRINTS; PR00237; GPCRHODOPSN.

R PRINTS; PR00237; GPCRHODOPSN.

R PROSITE; PS002290; IG_MHC; UNNONN 1.

DR PROSITE; PS002290; IG_MHC; UNNONN 1.

DR PROSITE; PS002290; IG_MHC; UNNONN 1.

KW G-POTCHIN COUPLED RECEPTION: RECEPTION: Transmembrane.

SEQUENCE 352 AA; 39624 MW; F240B68GD6BG368F CRC64;
                                                                                                              252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   85 MAMGEKWPFGWFLCKLIHIVVDINLFGSVFLIGFIALDRCICVLHPVWAQNHRTVSLAMK 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98 AV--ANWYFGNFLCKAVHVIYTVNLYSSVLILAFISLDRYLAIVHATNSQKPRKL-LAĒK 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    145 VI-VGPWILALVLTLPVFLFLTTVT-----IPNGDTYCTFNFASWGGTPEERLKV 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      194 AITMLTARGIIRFVIGFSLPMSIVAICYGLIAAKI-HKKGMIKSSRPLRVLTAVVASFFI 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38 RIFLPTIXSIIFLTGIVGNGLVILVMGYQKKLRSMTDKYRLHLSVADLLFVITLPFWAVD 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26 RILPLVVLGVTFVLGVLGNGLVIWVAGF-RMTRTVTTICYLNLALADFSFTATLPFLIVS 84
MAMGEKWPFGWFLCKLIHIVVDINLFGSVFLIGFIALDRCICVLHPVWAQNHRTVSLAMK
                                               145 VI-VGPWILALVLTLPVFLFLTTVT-----IPNGDTYCTFNFASWGGTPEERLKV
                                                               |: || || || :|| :| :| :|
150 VVYVGVWIPALLLTIPDFIFASVSEADDRFICDRFYPNDLWVVVFQFQ-------
                                                                                               194 AITMLTARGIIRFVIGFSLPMSIVAICYGLIAAKI-HKKGMIKSSRPLRVLTAVVASFFI
                                                                                                                                                                                                                                                                                                                                                                          Cercopithecus aethiops (Green monkey) (Grivet).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    107; Indels
                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23.2%; Score 421.5; DB 33.1%; Pred. No. 1e-28; iive 56; Mismatches 1
                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                               Cercopithecinae; Cercopithecus.
                                                                                                                                                                                                                 302 AKFKTSAQHAL-TSVSRGSS 320
                                                                                                                                                                                                 307 QDFRERLIHSLPTSLERALS 326
                                                                                                                                                                                                                                                                                                             01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-JUN-2002 (TrEMBLrel. 21.
                                                                                                                                                                                                                                                                                                                           (TrEMBLrel. 13, (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                     G-protein coupled receptor.
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                                                                                                                                                                                                                                                                                         PRELIMINARY;
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                                                                                                             || |: : : | |:: | :: | 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Presbytis entellus (Hanuman langur).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93 AV--ANWYFGNFLCKAVHVIYTVNLYSSVLILAFISLDRYLAIVHATNSQKPRKL-LAEK 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  85 MAMGEKWPFGWFLCKLIHIVVDINLFGSVFLIGFIALDRCICVLHPVWAQNHRTVSLAMK 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VI-VGPWILALVLTLPVFLFLTTVT------IPNGDTYCTFNFASWGGTPEERLKV 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RILPLVVLGVTFVLGVLGVLGNGLVIWVAGF-RMTRTVTTICYLNLALADFSFTATLPFLIVS 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Primates.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY)
-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
EMBL; AR172220; AAR89340.1; -.
InterPro; IPR0000276; GPCR_Rhodpsn.
InterPro; IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR01558; CHEMOKINER11.
PRINTS; PR01558; CHEMOKINER11.
PRINTS; PR01568; LYMPHOTACTRR.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS500250; FROTEIN_RECEP_F1_2; 1.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   253 CWFPFQLVALLGTVWLKEMLFYG-----KYKIIDILVNPTSSLAFFNSCLNPMLYVFVG
                                                                                   CWFPFQLVALLGTVWLKEMLFYG------KYKIIDILVNPTSSLAFFNSCLNPMLYVFVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      194 AITMLTARGIIRFVIGFSLPMSIVAICYGLIAAKI-HKKGMIKSSRPLRVLTAVVASFFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 347;
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150 VVYVGVWIPALLLTIPDFIFASVSEADDRYICDRFYPNDLWVVVFQFQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             307 QDFRERLIHSLPTSLERALS------EDSAPTNDTAANSAS 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   347 AA; 39145 MW; E96B660F1541515C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23.2%; Score 421; DB 6; L
llarity 31.8%; Pred. No. 1.1e-28;
Conservative 59; Mismatches 115;
                                                                                                                                                                                                                                                                                                                                                                                        347 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                      01-0cr-2000 (TrEMBLrel. 15, Created)
01-0cr-2000 (TrEMBLrel. 15, Last seq
01-UN-2002 (TrEMBLrel. 21, Last ann
Chemokine receptor CXCR4 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                          307 ODFRERLIHSLPTSLERALS 326
                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 110; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9574;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    56
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                            203
                                                                                                                                                                                                                                                                                                                                 RESULT 15
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us-09-944-807-2.rspt

Db 302 AKFKTSAQHAL-TSVSRGSSLKILSKGKRGGHSSVSTESESSSSHS 346

Search completed: December 16, 2002, 17:19:30 Job time : 36 secs

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GenCore version 5.1.3

Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 16, 2002, 17:16:27 ; Search time 15 Seconds

(without alignments)

688,496 Million cell updates/sec

Title: US-09-944-807-2
Perfect Score: 1817
Sequence: 1817
Sequence: 1 METNFSTPLNEYEEVSYESA.....TNDTAANSASPPAETELQAM 351
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 262574 seqs, 29422922 residues
```

otal number of hits satisfying chosen parameters: 262

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*

1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/pcTuS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/pcTuS_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 3, Appli	ω,	10,	34,	34,	348,	9, A	7	o,	٥	35,	Sequence 35, Appl	349,	350,	1, Ar	æ	Sequence 5, Appli	80	æ	11,	4,	7,	46,	Sequence 46, Appl	46,	46,	3,
ID	US-07-759-568-3	US-08-430-286A-8	US-08-458-970A-10	US-08-118-270-34	PCT-US93-08528-34	US-08-513-974B-348	US-08-458-970A-9	US-08-876-874-2	US-08-981-825-6	US-09-480-784-6	US-08-118-270-35	PCT-US93-08528-35	US-08-513-974B-349	US-08-513-974B-350	US-07-759-568-1	US-08-450-393A-8	US-08-390-000A-5	US-08-446-669-8	PCT-US95-00476-8	US-08-458-970A-11	US-08-148-209A-4	US-08-202-056-7	US-08-153-848-46	US-09-299-843A-46	US-09-088-337B-46	PCT-US93-11153-46	US-08-202-056-3
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Length	350	350	364	315	315	125	350	482	395	395	304	304	124	126	355	355	355	355	355	358	359	360	337	337	337	337	352
% Query Match	68.4	68.3	64.6	•	61.5	34.5	28.3	28.0	27.8	27.8	26.4	26.4	25.5	24.6	23.5	۳,	23.5	23.5	٠	•	ب	•	23.1	23.1	23.1	23.1	23.1
Score	1243.5	1240.5	1174.5	1117	1117	626.5	513	508.5	504.5	504.5	479	479	464	447	426.5	426.5	426.5	426.5	426.5	426.5			419.5		419.5		419.5
Result No.	1	7	m	4	ស	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27

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QY Dp

1, Appli	1, Appli	, Appli	, Appl	1, Appl	1, Appl.	1, Appl	Appl.	1, Appl	5, Appl	5, Appl:	5, Appl.	5, Appli	5, Appl1	2, Appl:	2, Appl	2, Appl:	5, Appli	
Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Seguence	Seguence	Sequence (Seguence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	
US-08-076-093A-4	US-08-701-265-4	US-08-284-586-4	US-08-805-478-4	US-08-802-627A-4	US-08-801-238-4	US-08-801-228-4	US-09-104-296-4	US-09-517-605-4	US-08-450-393A-6	US-08-446-669-6	PCT-US95-00476-6	US-08-041-219A-6	US-08-417-122-6	US-08-458-970A-2	US-09-146-980-2	US-08-430-286A-2	US-08-430-286A-5	
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352	352	352	352	352	352	352	352	352	352	352	352	359	359	355	362	356	356	
23.1	23.1	23.1	23.1	23.1	23.1	23.1	23.1	23.1	23.0	23.0	23.0	23.0	23.0	22.5	22.4	22.3	22.3	
419.5	419.5	419.5	419.5	419.5	419.5	419.5	419.5	419.5	418.5	418.5	418.5	418.5	418.5	409	407	406	406	
28	53	30	31	32	33	34	32	36	37	. 38	36	40	41	42	43	44	45	

ALIGNMENTS

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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 350;
US-07-759-568-3
Sequence 3, Application US/07759568
Sequence 3, Application US/07759568
GENERAL INFORMATION:
APPLICANT: Murphy, Philip M.
TITLE OF INVENTION: Cloning of cDNA Encoding a Functional TITLE OF INVENTION: Human Interleukin-8 Receptor NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 68.4%; Score 1243.5; DB 1; Length Best Local Similarity 68.6%; Pred. No. 8.4e-85; Matches 240; Conservative 37; Mismatches 72; Indels
                                                                                                                                                                                                                                                                                                                          ZIP: 20036-5601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/759,568
FILING DATE: 19910913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WTS/5683/91535/WBH
                                                                                                                                                                                                                ADDRESSEE: Cushman, Darby & Cushman
STREET: 1615 L Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: SCOCL, WASCON T.
RECISTRATION NUMBER: 26581
REFERENCE/DOCKET NUMBER: 4FS/:
TELEPHONE: 202-861-3000
TELEPHONE: 202-861-300
TELERAX: 202-82-0944
TELEX: 6714627 cush
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 350 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: peptide
                                                                                                                                                                                                                                      STREET: 1615 L St
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                            USA
                                                                                                                                                                                                                                                                                 STATE: D.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                         COUNTRY:
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LDRCICVLHPVWAQNHRTVSLAMKVIVGPWILALVLTLPVFLFLTTVTIPNGDTYCTFNF 180
                                                                           ASWGGTPEERLKVAITMLTARGIIRFVIGFSLPMSIVAICYGLIAAKIHKKGMIKSSRPL 240
                                                                                                                                       RVLTAVVASFFICWFPFQLVALLGTVWLKEMLFYGKYKIIDILVNPTSSLAFFNSCLNPM 300
                                                                                                                                                                                                68.3%; Score 1240.5; DB 4; Length 350;
68.6%; Pred. No. 1.4e-84;
                                                                                                                                                                                                                                          301 LYVFVGQDFRERLIHSLPTSLERALSEDSAPTNDTAANSASPPAETELQA 350
                                                                                                                                                                                                                                                           OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/430,286A
FILING DATE: 28-APR-1995
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Uhl, George R.
APPLICANT: Eppler, C. Mark
APPLICANT: Wang, Jai-Bel
TITLE OF INVENTION: Mu-Subtype Opioid Receptor
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 1.4e; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0646/1A843-US5
                                                                                                                                                                                                                                                                                                                                            Sequence 8, Application US/08430286A
Patent No. 6225080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Robinson, Joseph R.
REGISTATION UNDRER: 33,448
REFERENCE/DOCKET UNDRER: 0646,
TELECOMMUNICATION INFORMATION:
TELEFAX: 212-52-7700
TELEFAX: 212-53-770
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 350 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Darby & Darby PC
STREET: 805 Third Avenue
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
FRAGMENT TYPE: N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IMMEDIATE SOURCE:
CLONE: F-PEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: New COUNTRY: US ZIP: 10022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM:
                                                                                                                                                                                                                                                                                                                             JS-08-430-286A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-430-286A-8
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Matches 240;
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                                                                                                                                                                                                                                                RVLTAVVASFFICWFPFQLVALLGTVWLKEMLFYGKYKIIDILVNPTSSLAFFNSCLNPM 300
                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                  TICYLNLALADFSFTATLPFLIVSMAMGEKWPFGWFLCKLIHIVVDINLFGSVFLIGFIA
                                                                                                                                                                                                                               181 ASWGGTPEERLKVAITMLTARGIIRFVIGFSLPMSIVAICYGLIAAKIHKKGMIKSSRPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 METNFSTPLNEYE------EVSYESAGYTVLRILPLVVLGVTFVLGVLGNGLVIWVAG
                                                                                                                                                                                                                                                                                                                                                                                                                   301 LYVFVGQDFRERLIHSLPTSLERALSEDSAPTNDTAANSASPPAETELQA 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64.6%; Score 1174.5; DB 2;
64.6%; Pred. No. 1.1e-79;
ive 38; Mismatches 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CONTESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESSEE: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 53.0
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/09234
FILING DATE: 16 AUG 1994
ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISSTRATION NUMBER: 33.073
FELECOMMULICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEPHONE: 201-994-1700
TELEFAX: 201-994-174
INPORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 364 amino acids
...... smino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/458,970A FILING DATE: June 2, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-458-970A-10; Sequence 10, Application US/08458970A; Patent No. 5861272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3: 3.5 INCH DISKETTE IBM PS/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: LI, ET AL.
TITLE OF INVENTION: C5a Receptor
NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 64.6
Matches 237; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: 3,5 INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 6 BECKER F
CITY: ROSELAND
STATE: NEW JERSEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                             121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ŏ
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Length 315;

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Sequence 34, Application US/08118270
Patent No. 5508384
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Murphy, Randall B.
APPLICANT: Schuster, David I.
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIWARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Mashington
STATE: D.C.
COUNTRY: USA
                                               113 VFLIGFIALDRCICVLHPVWAQNHRTVSLAMKVIVGPWILALVLTLPVFLFLTTVTIPN- 171
                                                                                                                                                                                       172 ----GDTYCTFNFASWGGTPEERLKVAITMLTARGIIRFVIGFSLPMSIVAICYGLIAAK 227
                                                                                                                                                                                                                                                            228 IHKKGMIKSSRPLRVLTAVVASFFICWFPFQLVALLGTVWLKEMLFYGKYKIIDILVNPT 287
                                                                                                                                                                                                                                                                                                                                 SSLAFFNSCLNPMLYVFVGQDFRERLIHSLPTSLERALSEDSAPTNDTAAN---SASPPA 344
298 SPLAFFNSCLNPMLYVFWGQDFRERLIHSLPASLERALTEDSAQTSDTGTNLGTNSTSLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC comparible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTONELYAGENT INFORMATION:
NAME: TOWNSEND, KEVIN G.
REGISTRATION NUMBER: 34,033
REFENDE/DOCKET NUMBER: MURPHY=2A
TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UMBER: US/08/118,270
09-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 315 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                   ETELQAM 351
                                                                                                                                                                                                                                                                                                                                                                                                                                     ENTLNAM 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20004
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87 MCEKWPFGWFLCKLIHIVVDINLFGSVFLIGFIALDRCICVLHPVWAQNHRTVSLAMKVI 146
                                                                                                                                                                147 VGPWILALVLTLPVFLFLFTVTIPNGDTYCTFNFASWGGTPEERLKVAITMLTARGIIRF 206
                                                                                                                                                                                                                                          207 VIGESLPMSIVAICYGLIAAKIHKKGMIKSSRPLRVLTAVVASFFICWFPFQLVALLGTV 266
                                                                                                                                                                                                                                                                                                                                                                 267 WLKEMLFYGKYKIIDILVNPTSSLAFFNSCLNPMLYVFVGQDFRERLIHSLPTSLERALS 326
                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 34, Application PC/TUS9308528
GENERAL INFORMATION:
APPLICANT: New YORK University
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:
                                                                           86
                                                                                            27 ILPLVVLGVTFVLGVLGNGLVIWVAGFRMTRTVTTICYLNLALADFSFTATLPFLIVSMA
                                       10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 315;
                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PATENTIA RELEASE #1.0, Version #1.25
SOFTWARE: PATENTIA RELEASE #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08528
FILING DATE: 09-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
Score 1117; DB 1;
Pred. No. 1.7e-75;
7: Mismatches 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
                                     37; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61.5%; Score 1117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MURPHY-2 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                         EDSAPTNDTAANSASPPAETELQA 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EDSTQTSDTATNSTLPSAEVALQA 314
 61.58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 24863
INFORMATION FOR SEQ 1D NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 315 amino acida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                315 amino acids
 Query Match
Best Local Similarity 67.33
Matches 218; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: 202-02-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: D.C. COUNTRY: US
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PCT-US93-08528-34
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125 ICVLHPVWAQNHRTVSLAMKVIVGPWILALVLTLPVFLFLTTVTIPNGDTYCTFNFASWG 184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 125;
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___AUDRESS:
___SEE: CARELLA, BYRNE, BAIN, GILFILLAN,
STREET: 6 BECKEN, STEWART & OLSTEIN
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 0706^
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34.5%; Score 626.5; DB 3 99.2%; Pred. No. 1.1e-39; iive 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 9, Application US/08458970A
Patent No. 5861272
GENERAL INFORMATION:
TITLE OF INVENTION: C5a Receptor
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESSE:
ADDRESSEE: CARELLA, BYRNE, BAIN,
ADDRESSEE: CECCHI, STEWART & OLST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERPECT 5.1
CURRENT APPLICATION DATA:
                                                                             APPLICATION NUMBER: JP 6-236357
FILING DATE: 30-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-236356
FILING DATE: 30-SEP-1994
                                                                                                                                           APPLICALLY
FILING DATE: 30-SEF
PRIOR APPLICATION DATA:
APPLICATION UMBER: JP 6-189274
APPLICATION 11-AUG-1994
                                                                                                                                                                                                                      FILING DATE: 11-ANG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189273
FILING DATE: 11-ANG-1945
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189272
                                                                                                                                                                                                                                                                                                                                            FILING DATE: 11-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: RESTICK, David S.
REGISTRATION NUMBER: 34,235
                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 45
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 348:
                       JMBER: JP 6
02-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 125 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best_Local Similarity 99.2
Matches 124; Conservative
                     APPLICATION NUMBER: : FILING DATE: 02-NOV-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          244 TAVVA 248
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                                                                                                                                      147 VGPWILALVLTLPVFLFLTTVTIPNGDTYCTFNFASWGGTPEERLKVAITMLTARGIIRF 206
                                                                                                                                                                                                                                            207 VIGFSLPMSIVAICYGLIAAKIHKKGMIKSSRPLRVLTAVVASFFICWFPFQLVALLGTV 266
                                                                                                                                                                                                                                                                                                                                                                                     267 WLKEMLFYGKYKIIDILVNPTSSLAFFNSCLNPMLYVFVGQDFRERLIHSLPTSLERALS 326
                                                                                27 ILPLVVLGVTFVLGVLGVLGNGLVIMVAGFRMTRTVTTICYLNLALADFSFTATLPFLIVSMA 86
Best Local Similarity 67.3%; Pred. No. 1.7e-75;
Matches 218; Conservative 37; Mismatches 59; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Fujii, Ryo
APPLICANT: Obtaki, Tetsuya
APPLICANT: Obtaki, Tetsuya
APPLICANT: Obji, Kazuhiro
APPLICANT: Obji, Kazuhiro
TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
TITLE OF INVENTION: PRODUCTION, AND USE THEREOF
CORRESPONDENCES: 380
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/513,974B
FILING DATE: 14-SEP-1995
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 14-SEP-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DCT/JP95/01599
FILING DATE: 10-AUG-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
PRYOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-007177
FILING DATE: 20-JAN 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-326611
FILING DATE: 28-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 348, Application US/08513974B Patent No. 6114139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: JP 7-093989
FILING DATE: 19-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             UMBER: JP 7-057186
16-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   327 EDSAPTNDTAANSASPPAETELQA 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          291 EDSTQTSDTATNSTLPSAEVALQA 314
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Hosoya, Masaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Hinuma,
APPLICANT: Hosoya,
APPLICANT: Fujii,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-513-974B-348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
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178 FNFA-----SW------ 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  234 FQRPSADSLPRGSARLTSQNLYSNVFKPADVVSPKIPSGFPIEDHETSPLDNSDAFLSTH 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :: :| :| :| : | : | : | 397 GVLSLLTDPETPLGKTLMSWDHVCIALASANSCFNPFLYALLGKDFRKKARQSIQGILEA 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58 TVTTICYLNLALADFSFTATLPFLIVSMAMGEKWPFGWFLCKLIHIVVDINLFGSVFLIG 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                118 FIALDRCICVLHPVWAQNHRTVSLAMKVIVGPWILALVLTLPVFLFLTTVTIPNGDTYCT 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----AITMLTARGIIRFVIGFSLPMSIVA 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             294 LKLFPSASSNSFYESELPQGFQDYYNLGQFTDDDQVPTPLVAITITRLVVGFLLPSVIMI 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               278 KIIDILVNPTS-----SLAFFNSCLNPMLYVFVGQDFRERLIHSLPTSLER 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           219 ICYGLIAAKIHKKGMIKS-SRPLRVLTAVVASFFICWFPFQLVALLGTVWLKEMLFYGKY 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 EIN----FSTPLNEYEEVSYESAGYTVLRILPLVVLGVTFVLGVLGNGLVIWVAGFRMTR 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 28.0%; Score 508.5; DB 2; Length 482; Best Local Similarity 26.6%; Pred. No. 2.2e-30; Matches 134; Conservative 59; Mismatches 117; Indels 193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENY APPLICATION DATA:
APPLICATION NUMBER: US/08/876,874
                                                                                                                                                                         PILING DATE:
CLASSTRICATION: 536
PROR APPLICATION DATA:
PREDICATION NUMBER: 60/019,627
FILING DATE: 16-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: PRESTIA, PAUL F
REGISTRATION NUMBER: 23,031
REPERRENCE/PROCKET NUMBER: P5050
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AFSEELTRSTHCPSNNVISERNS 479
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 482 amino acids
TYPE: amino acid
                                                                             Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: protein US-08-876-874-2
                                                       COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                             MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   191 LKV----
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           COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    125 LLIATISADRFLLVFKPIWCQNFRGAGLAWIACAVAWGLALLLTIPSFLYRVV----RE 179
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229 TWSRRATRSTKTLKVVVAVVASFFIFWLPYQVTGIM------MSFLEPSSPTFILLINKL 281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            288 SSL----AFFNSCLNPMLYVFVGQDFRERLIHSLPTSLERALSEDSA------PTND 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28.2%; Score 513; DB 2; Length 350; 33.6%; Pred. No. 7.3e-31; ive 60; Mismatches 129; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/08876874

Patent No. 5942405

GENERAL INFORMATION:
APPLICANT: Bergsma, Derk
APPLICANT: Kumar, Chandrika
APPLICANT: Kumar, Chandrika
TITLE OF INVENTION: THERAPEUTIC AND SCREENING
TITLE OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:
APPLICATION NUMBER: US/08/458,970A
FILING DATE: June 2, 1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/09234
FILING DATE: 16 AUG 1994
ATTORNEY AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRANTON UNMBER: 325800-353
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 350 mmino acids
TYPE: amino acid
TYPE: amino acid
TYPE: ATTORNEYS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: RATNER & PRESTIA
STREET: P.O. BOX 980
CITY: VALLEY FORGE
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 28.2
Best Local Similarity 33.6
Matches 122; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                          linear
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US-08-876-874-2
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11;

Gaps

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129 HPVWAQNHRTVSLAMKVIVGPWILALVLTLPVFLFLTTVTIPNGDTYCTFNFASWGGTPE 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DRDATCNSRQAALAVSKFLLAFLVPLAIIASSHAAVSLRLQHRGRRRPGRFVRLVAAVVA 253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13 BEVS-YESAGYTVLRIL---PLVVLGVTFVLGVLGNGLVIWVAGFRMTRTVTTICYLNLA 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15 EQMSRLQSHSNTSIRYIDHAAVLLHGLASLLGLVENGVILFVVGCRMRQTVVTTWVLHLA
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                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: PROTEIN SPECIFIC TO HUMAN
Th2, GENE (B19) ENCODING THE SAME, AND
  306 LICPDMLRKLRRSLRTVLESVLVDDSELGGAGSSRRRRTSSTARSASPLA 355
                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Knobbe, Martens, Olson & Bear STREET: 620 Newport Center Drive 16th Floor CITY: Newport Beach STATE: CA STATE: CA COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 27.8%; Score 504.5; DB 4; Best Local Similarity 34.0%; Pred. No. 3.5e-30; Matches 119; Conservative 75; Mismatches 129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: MSHIM4.001APC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IEM COMPATIBLE
COMPUTER: IEM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FRASEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/480,784
FILING DATE: 10-43m-2000
CLASSIFICATION CURROWN>
PRIOR APPLICATION NUMBER: 08/981,825
FILING DATE: <URROWN>
FILING DATE: <URROWN>
APPLICATION NUMBER: 08/981,825
FILING DATE: <URROWN>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 6: US-09-480-784-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
                                                                                                                 Sequence 6, Application US/09480784 Patent No. 6166186 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 714-760-0404
TELEFAX: 714-760-9502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 395 amino acids
                                                                                                                                                                                            APPLICANT: OGAWA, KAZUYAUKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                TAKANO, SYOICHI
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INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
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                                                                        RESULT 10
US-09-480-784-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            189 ERLKVAITMLTARGIIRFVIGFSLPMSIVAICYGLIAAKIHKKGMIKSSRPLRVLTAVVA 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     249 SFFICWFPFQLVALL ---- GTVWLKEMLFYGKYKIIDILVNPTSSLAFFNSCLNPMLYV 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15 EQMSRLQSHSNTSIRYIDHAAVLLHGLASLLGLVENGVILFVVGCRMRQTVVTTWVLHLA 74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
27.8%; Score 504.5; DB 3; Length 395;
Best Local Similarity 34.0%; Pred. No. 3.5e-30;
Matches 119; Conservative 75; Mismatches 129; Indels 27
                                                                                                                                                                                  TITLE OF INVENTION: PROTEIN SPECIFIC TO HUMAN
TITLE OF INVENTION: Th2, GENE (B19) ENCODING THE SAME, AND
NUMBER OF SEQUENCES:
GORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  304 FVGQDFRERLIHSLPTSLERALSEDS------APTNDTAANSASPPA 344
                                                                                                                                                                                                                                                                              ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: MSHIM4.001APC TELECOMMUNICATION INFORMATION: TELEPHONE: 714-760-0404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: DOS
SOFTWARE: FRSKSEQ VERSION 1.5
SUSRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/981,825
                     Sequence 6, Application US/08981825 Patent No. 6040426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34,115
                                                                 GENERAL INFORMATION:
APPLICANT: OGAWA, KAZUYAUKI
APPLICANT: TANAKA, KAZUYA
APPLICANT: NAGATA, KINYA
APPLICANT: TAKANO, SYOICHI
                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          395 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Altman, Daniel E
REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 714-760-9502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 92660
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US-08-981-825-6
                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH:
                                                                                                                                                                                                                                                                                                                                                    STATE:
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27; Gaps

Indels

Length 395;

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261 ALLGTVWLKEMLFYGKYKIIDILVNPTSSL----AFFNSCLNPMLYVFVGQ-DFRERLIH 315
                       Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26.4%; Score 479; DB 5; I
33.8%; Pred. No. 2.1e-28;
iive 56; Mismatches 109;
                                                                                                 268 SLPSLLRNVLTEESVVRESKSFTRSTVDTMA 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: MURPHY=2 PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORFIATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Ve CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT/US93/08528 FILING DATE: 09-SEP-1993
                                                                            SLPTSLERALSEDSA-----PTNDTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 09-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Townsend, Kevin G. REGISTRATION NUMBER: 34,033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   167 -AIVRLVLGFLWPLLTLTICY--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         304 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 26.4%
Best Local Similarity 33.8%
Matches 112; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 248633
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                      20004
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                                                                                                                                                                                         PCT-US93-08528-35
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 87 MGEKWPFGWFLCKLIHIVVDINLFGSVFLIGFIALDRCICVLHPVWAQNHRTVSLAMKVI 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   147 VGPWILALVLTLPVFLFLTTVTIPNGDTY-----CTFNFASWGGTPEERLKVAITMLTA 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         201 RGIIRFVIGFSLPMSIVAICYGLIAAKIHKKGMIKSSRPLRVLTAVVASFFICWFPFQLV 260
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                                                                                                                                                                                                                                        APPLICANT: Murphy, Randall B.
APPLICANT: Schuster, David I.
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
CORRESPONDENCES: 348
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 ILALVIFAVVFLVGVLGNALVVWVTAFEAKRTINAIWFLNIAVADFLSCLALPILFTSIV 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27 ILPLVVLGVTFVLGVLGNGLVIWVAGFRMTRTVTTICYLNLALADFSFTATLPFLIVSMA 86
                                                                            ---APTNDTAANSASPPA 344
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                          E: BROWDY AND NEIMARK 419 Seventh Street, N.W., Suite 300
:| :| | |: :: | 254 AFALCWGPYHVFSLLEARAHANPGLRPLVWRG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/118,270 FILING DATE: 09-SEP-1993 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/943,236 FILING DATE: 10-SEP-1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                      304 FVGQDFRERLIHSLPTSLERALSEDS---
                                                                                                                                                                                     Sequence 35, Application US/08118270 Patent No. 5508384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MURPI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 248633
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 304 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 26.4%
Best Local Similarity 33.8%
Matches 112; Conservative
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MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                  STREET: 412 CITY: Washington
                                                                                                                                                                                                                           GENERAL INFORMATION:
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                                                                                                                                                RESULT 11
US-08-118-270-35
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87 MGEKWPFGWFLCKLIHIVVDINLFGSVFLIGFIALDRCICVLHPVWAQNHRTVSLAMKVI 146 147 VGPWILALVLTLPVFLFLFTVTIPNGDTY-----CTFNFASWGGTPEERLKVAITMLTA 200 Sequence 35, Application PC/TUS9308528
GENERAL INFORMATION:
APPLICANT: New York University
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Mashington 261 ALLGTVWLKEMLFYGKYKIIDILVNPTSSL----AFFNSCLNPMLYVFVGQ-DFRERLIH 315 Gaps 27 ILPLVVLGVTFVLGVLGVLGNGLVIWVAGFRMTRTVTTICYLNLALADFSFTATLPFLIVSMA 86 122 AVAWGIALLLTIPSFLYRVV----REEYFPPKVLCGCDYSH-----DKRRERAV--------TIRSTKTLKVVVAVVASFFIFWLPYQVT RGIIRFVIGFSLPMSIVAICYGLIAAKIHKKGMIKSSRPLRVLTAVVASFFICWFPFQLV 54; Length 304;

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125 ICVLHPVWAQNHRTVSLAMKVIVGPWILALVLTLPVFLFLTTVTIPNGDTYCTFNFASWG 184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Fujii, Ryo
APPLICANT: Ohtaki, Tetsuya
APPLICANT: Ohtaki, Tetsuya
APPLICANT: Pukusumi, Shoji
APPLICANT: Fukusumi, Shoji
APPLICANT: Ohgi, Razuhiro
TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
TITLE OF INVENTION: PRODUCTION, AND USE THEREOF
TITLE OF SEQUENCES: 380
CORRESPONDENCES: 380
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP STREET: 130 Water Street
CITY: Boston
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: EN PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/513,974B
FILING DATE: 14-SEP-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: PCT/JP95/01599
FILING DATE: 10-MG-1995
PRICH APPLICATION DATA:
APPLICATION NUMBER: PCT/JP95/01599
PRICH APPLICATION DATA:
APPLICATION NUMBER: US/09999
                                                                                                                                                                                                                                                                                                                       Query Match
25.5%; Score 464; DB 3;
Best Local Similarity 69.4%; Pred. No. 1.1e-27;
Matches 86; Conservative 16; Mismatches 22;
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FILING DATE: 19-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-057186
FILING DATE: 16-MAR-1995
PRIOR APPLICATION NUMBER: JP 7-007177
FILING DATE: 20-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 350, Application US/08513974B Patent No. 6114139
                                                                                  TELEFAX: 617-53-6440
INFORMATION FOR SEQ ID NO: 349:
SEQUENCE CHARACTERISTICS:
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 45
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEPRAX: 617-523-6440
                                                                                                                                                             i: 124 amino acids amino acids
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APPLICANT: Hosoya, Masaki
                                                                                                                                                                                                                                                     ; MOLECULE TYPE: peptide US-08-513-974B-349
                                                                                                                                                                                                                                    linear
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TOPOLOGY: 111
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APPLICANT: HOSOYA, MASAKI
APPLICANT: FUJII, RYO
APPLICANT: Obtaki, Tetsuya
APPLICANT: Obji, Razuhiro
APPLICANT: Obji, Razuhiro
TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
TITLE OF INVENTION: PRODUCTION, AND USE THEREOF
NUMBER OF SEQUENCES: 380
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: FLORM:
MEDIUM TYPE: FLORM:
MEDIUM TYPE: FLORM:
MEDIUM TYPE: FLORM:
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CURRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARING SYSTEM: PC-DOS/MS-DOS
SOFTWARING PAPLICATION DATA:
APPLICATION NUMBER: US/08/513,974B
FILING DATE: 10-AUG-1995
FILING APPLICATION DATA:
APPLICATION NUMBER: P7 -093989
FILING DATE: 19-AUG-1995
FILING DATE: 19-AUG-1995
FILING DATE: 19-AUG-1995
FILING DATE: 16-AMR-1995
FILING DATE: 16-AMR-1995
FILING DATE: 10-AUG-1995
FILING DATE: 20-JAN-1995
FILING DATE: 20-JAN-1994
FILING DATE: 20-JAN-1994
FILING DATE: 20-NOV-1994
FILING NAMBER: JP 6-236357
FILING DATE: 30-NOV-1994
FILING NAMBER: JP 6-236357
FILING NAMBER: JP 6-236357
FILING NAMBER: JP 6-236357
FILING NAMBER: JP 6-236357
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                                                                    316 SLPTSLERALSEDSA-----PTNDTAA 337
                                                                                                          268 SLPSLLRNVLTEESVVRESKSFTRSTVDTMA 298
                                                                                                                                                                                                                      Sequence 349, Application US/08513974B
Patent No. 6114139
GENERAL INFORMATION:
APPLICANT: Hinuma, Shuji
APPLICANT: Hosoya, Masaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: JP 6-236357
FILING DATE: 30-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-236356
FILING DATE: 30-SEP-1994
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APPLICATION NUMBER: JP 6-189274
FILING DATE: 11-AUG-1994
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APPLICATION NUMBER: JP 6-189272
FILING DATE: 11-AUG-1994
ATTORNEY/AGENT INFORMATION:
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11-AUG-1945
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APPLICATION NUMBER: 3
FILING DATE: 11-AUG-1
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US-08-513-974B-349
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: MA
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single
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                                                                                                                                                                                                                                                                                                                                                                           linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 WTEDPAEKLKVAISMEMVRGIIRFIIGFSTPMSIVAVCYGLIATKIHRQGLIKSSRPLRV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           125 ICVLHPVWAQNHRTVSLAMKVIVGPWILLALVLTLPVFLFLTTVTIPN--GDTYCTFNFAS 182
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Patent No. 5374506
GENERAL INFORMATION:
APPLICANT: Murphy, Philip M.
TITLE OF INVENTION: Cloning of cDNA Encoding a Functional
TITLE OF INVENTION: Human Interleukin-8 Receptor
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 24.6%; Score 447; DB 3; Length 12: Best Local Similarity 69.0%; Pred. No. 2e-26; Matches 87; Conservative 16; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Cushman, Darby & Cushman
STREET: 1615 L Street, N.W.
                                                                   FILING DATE: 10-NOV-1994
PRIOR APPLICATION NUMBER: 17 6-270017
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 17 6-236357
FILING DATE: 30-SEP-1994
PRIOR APPLICATION NUMBER: 17 6-236356
FILING DATE: 30-SEP-1994:
APPLICATION NUMBER: 17 6-189274
FILING DATE: 11-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 17 6-189273
FILING DATE: 11-AUG-1994
ATTORNEY/AGRATION:
ATTORNEY/AGRATION:
ATTORNEY/AGRATION:
                    APPLICATION NUMBER: JP 6-326611
                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Resnick, David S.
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 45753
TELECOMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 350:
SEQUENCE CHARACTERISTICS:
                                  FILING DATE: 28-DEC-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               126 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                617-523-6440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: peptide
PRIOR APPLICATION DATA:
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LSFVVA 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    243 LTAVVA 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-513-974B-350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Wash
STATE: D.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-07-759-568-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121
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241 RVLTAVVASFFICWFPFQLVALLGTVWLKEML--FYGKYKIIDILVNPTSSLAFFNSCLN 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  72 FSFTATLPFLIVSMAMGEKWPFGWFLCKLIHIVVDINLFGSVFLIGFIALDRCICVLHPV 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90 LLFALTLPIWAASKVNG--WIFGTFLCKVVSLLKEVNFYSGILLLACISVDRYLAIVHAT 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      132 WAQNHRTVS----LAMKVIVGPWILALVLTLPVFLFLTTVTIPNGDTYC----TFNFASW 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35 EPESLEINKYFVVIIYALV----FLLSLIGNSLVMLVILYSRVGRSVTDVYLLNLALAD 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13 EEVSYESAGYTVLRILPLVVLGVTFVLGVLGNGLVIWVAGF-RMTRTVTTICYLNLALAD 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                184 GGTPEERLKVAITMLTARGIIRFV---IGFSLPMSIVAICYGLIAAKIHKKGMIKSSRPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     299 PMLYVFVGQDFRERLIHSLPTSLERALSEDSAPTNDTAANSASPPAET 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 23.5%; Score 426.5; DB 1; Best Local Similarity 32.5%; Pred. No. 1.8e-24; Matches 113; Conservative 59; Mismatches 131;
                                                                                                                                                                                                                       WTS/5683/91535/WBH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Search completed: December 16, 2002, 17:18:50 Job time : 17 secs
                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/759,568
FILING BARE: 1991033
CLASSIFICATION: 435
ATORNEY AGENT INFORMATION:
NAME: SCOCK, WALSON T.
RECISTRATION NUMBER: 26891
RECISTRATION NUMBER: 26891
TELEPHONE: 202-861-3000
TELEFAX: 202-861-3000
PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                    TELEX: 6714627 cush
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
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AMINO ACID
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